FOOTPRINTING HYDROXYL RADICAL DNA

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=> d his

     (FILE 'HOME' ENTERED AT 11:55:51 ON 14 MAR 2002)
               SET COST OFF

     FILE 'REGISTRY' ENTERED AT 11:56:09 ON 14 MAR 2002
L1          3040 S .C.{2-4}C.{2-3}F.....L..H...H/SQSP
               SAV TEMP L1 HOPE424488/A
               E TGEK/SQEP
L2             1 S E3
L3             1 S E6

     FILE 'HCAPLUS' ENTERED AT 11:59:00 ON 14 MAR 2002
L4          1091 S L1
L5             8 S L2 OR L3
L6             6 S TGEK OR TGEKP
L7             7 S L4 AND L5,L6
L8           780 S L4 AND (ZN OR ZINC)(L)FINGER
L9            18 S L4 AND ALPHA(L)(HELICAL OR HELIX)
L10            3 S L4 AND QUAD?
L11          450 S L4 AND (DNA OR NUCLEIC ACID)(L)BINDING(L)PROTEIN
L12           40 S L4 AND CYS2(L)HIS2
L13            4 S L4 AND CYS()2(L)HIS()2
L14           32 S L11 AND L12,L13
L15          398 S L11 AND L8
L16           11 S L15 AND L9,L10
L17           61 S L5-L7,L9,L10,L14,L16
               E WO98-53060/AP,PRN
               E WO9853060/PN
L18            1 S E3
               E WO98-GB1516/AP,RPN
               E WO98-GB1516/AP,PRN
L19            1 S E3,E4
L20            1 S L18,L19
               E CHOO Y/AU
L21           71 S E3-E14
               E  KLUG A/AU
L22          191 S E3,E4
               E ISALAN M/AU
L23           15 S E4
L24           15 S L4 AND L18-L23
L25           15 S L24 AND L8
L26           12 S L24 AND L11
L27            6 S L24 AND L9,L10,L12,L13
L28            5 S L27 AND L26
L29            6 S L27 AND L25
L30            6 S L28,L29
L31            5 S L30 NOT PROTON/TI
L32            5 S L20,L31
L33           10 S L24-L30 NOT L32
L34           66 S L4 AND (DNA OR NUCLEIC ACID)(L)BINDING(L)(PEPTIDE OR POLYPEPT
L35           45 S L34 AND L8
L36            8 S L34 AND L12,L13
L37           90 S L17,L32,L35,L36
L38           93 S L33,L37
L39          600 S L4 AND (PD<=19980526 OR PRD<=19980526 OR AD<=19980526)
L40           59 S L39 AND L38
               E DNA BINDING PROTEIN/CT
               E DNA-BINDING PROTEIN/CT
               E E4+ALL
L41         7172 S E1,E2,E3
               E E2+ALL
L42           52 S E3
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                E DNA-BINDING PROTEIN/CT
                E E4+ALL
                E E3+ALL
L43          108 S L41,L42 AND L39
L44          266 S L39 AND L11,L34
L45          266 S L43,L44
L46          242 S L45 AND (ZN OR ZINC)(L)FINGER
L47           23 S L46 AND L12,L13
L48           33 S RECOGNI? AND L46
                E MOLECULAR RECOGNITION/CT
                E E3+ALL
L49            7 S E2,E1+NT AND L46
L50            9 S E6+NT AND L46
L51            3 S RECOGNITION CODE AND L46
L52           35 S L47,L49-L51,L32
L53           20 S L47,L48 NOT L52
L54            6 S L53 AND (CONSEN? OR MOTIF)/TI
L55            2 S L54 AND (BINDING PROTEIN)/TI
L56           37 S L52,L55
L57           37 S L56 AND L4-L56

     FILE 'HCAPLUS' ENTERED AT 12:25:10 ON 14 MAR 2002

     FILE 'BIOSIS' ENTERED AT 12:25:41 ON 14 MAR 2002
                E CHOO Y/AU
L58           96 S E3-E12,E14
                E QUE L22
                E KLUG A/AU
L59          155 S E3,E4
                E ISALAN M/AU
L60            7 S E4
L61            0 S L1
L62            0 S L2
L63          237 S L58-L60
L64        49215 S (DNA OR NUCLEIC ACID)(L)BINDING(L)(PROTEIN OR PEPTIDE OR POLY
L65           27 S L63 AND L64
L66           16 S L65 AND PY<=1998
L67            0 S L66 AND QUAD?
L68            0 S L66 AND TETRA?
L69            1 S L66 AND TERT?
L70           13 S L66 AND (ZN OR ZINC)(L)FINGER
L71            3 S L66 NOT L70
L72            1 S L71 AND DESIGNING
L73           14 S L70,L72 AND L58-L72

     FILE 'HCAPLUS, BIOSIS' ENTERED AT 12:29:33 ON 14 MAR 2002
L74           49 DUP REM L57 L73 (2 DUPLICATES REMOVED)
                SET COST ON
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Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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=> d his

     (FILE 'HOME' ENTERED AT 11:55:51 ON 14 MAR 2002)
                SET COST OFF

     FILE 'REGISTRY' ENTERED AT 11:56:09 ON 14 MAR 2002
L1           3040 S .C.{2-4}C.{2-3}F.....L..H...H/SQSP
                  SAV TEMP L1 HOPE424488/A
                  E TGEK/SQEP
L2              1 S E3
L3              1 S E6

     FILE 'HCAPLUS' ENTERED AT 11:59:00 ON 14 MAR 2002
L4           1091 S L1
L5              8 S L2 OR L3
L6              6 S TGEK OR TGEKP
L7              7 S L4 AND L5,L6
L8            780 S L4 AND (ZN OR ZINC)(L)FINGER
L9             18 S L4 AND ALPHA(L)(HELICAL OR HELIX)
L10             3 S L4 AND QUAD?
L11           450 S L4 AND (DNA OR NUCLEIC ACID)(L)BINDING(L)PROTEIN
L12            40 S L4 AND CYS2(L)HIS2
L13             4 S L4 AND CYS()2(L)HIS()2
L14            32 S L11 AND L12,L13
L15           398 S L11 AND L8
L16            11 S L15 AND L9,L10
L17            61 S L5-L7,L9,L10,L14,L16
                  E WO98-53060/AP,PRN
                  E WO9853060/PN
L18             1 S E3
                  E WO98-GB1516/AP,RPN
                  E WO98-GB1516/AP,PRN
L19             1 S E3,E4
L20             1 S L18,L19
                  E CHOO Y/AU
L21            71 S E3-E14
                  E  KLUG A/AU
L22           191 S E3,E4
                  E ISALAN M/AU
L23            15 S E4
L24            15 S L4 AND L18-L23
L25            15 S L24 AND L8
L26            12 S L24 AND L11
L27             6 S L24 AND L9,L10,L12,L13
L28             5 S L27 AND L26
L29             6 S L27 AND L25
L30             6 S L28,L29
L31             5 S L30 NOT PROTON/TI
L32             5 S L20,L31
L33            10 S L24-L30 NOT L32
L34            66 S L4 AND (DNA OR NUCLEIC ACID)(L)BINDING(L)(PEPTIDE OR POLYPEPT
L35            45 S L34 AND L8
L36             8 S L34 AND L12,L13
L37            90 S L17,L32,L35,L36
L38            93 S L33,L37
L39           600 S L4 AND (PD<=19980526 OR PRD<=19980526 OR AD<=19980526)
L40            59 S L39 AND L38
                  E DNA BINDING PROTEIN/CT
                  E DNA-BINDING PROTEIN/CT
                  E E4+ALL
L41          7172 S E1,E2,E3
                  E E2+ALL
L42            52 S E3
                  E DNA-BINDING PROTEIN/CT
                  E E4+ALL
                  E E3+ALL
```

```
L43          108 S L41,L42 AND L39
L44          266 S L39 AND L11,L34
L45          266 S L43,L44
L46          242 S L45 AND (ZN OR ZINC)(L)FINGER
L47           23 S L46 AND L12,L13
L48           33 S RECOGNI? AND L46
                 E MOLECULAR RECOGNITION/CT
                 E E3+ALL
L49            7 S E2,E1+NT AND L46
L50            9 S E6+NT AND L46
L51            3 S RECOGNITION CODE AND L46
L52           35 S L47,L49-L51,L32
L53           20 S L47,L48 NOT L52
L54            6 S L53 AND (CONSEN? OR MOTIF)/TI
L55            2 S L54 AND (BINDING PROTEIN)/TI
L56           37 S L52,L55
L57           37 S L56 AND L4-L56

=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 12:25:10 ON 14 MAR 2002
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FILE COVERS 1907 - 14 Mar 2002  VOL 136 ISS 11
FILE LAST UPDATED: 12 Mar 2002  (20020312/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

CAS roles have been modified effective December 16, 2001. Please
check your SDI profiles to see if they need to be revised. For
information on CAS roles, enter HELP ROLES at an arrow prompt or use
the CAS Roles thesaurus (/RL field) in this file.

The P indicator for Preparations was not generated for all of the
CAS Registry Numbers that were added to the CAS files between 12/27/01
and 1/23/02.  As of 1/23/02, the situation has been resolved.  Searches
and/or SDIs in the H/Z/CA/CAplus files incorporating CAS Registry
Numbers with the P indicator executed between 12/27/01 and 1/23/02 may
be incomplete.  See the NEWS message on this topic for more information.

=> d l57 bib abs hitrn retable tot

L57  ANSWER 1 OF 37  HCAPLUS  COPYRIGHT 2002 ACS
AN   2002:51500  HCAPLUS
DN   136:114558
TI   Zinc finger synthetic polypeptides
     binding to telomeric G quadruplex DNA
IN   Choo, Yen; Isalan, Mark; Liu, Xiaohai; Patel, Sachin;
     Balasubramanian, Shankar
PA   Sangamo Biosciences, Inc., USA; Cambridge University Technical Services
     Ltd.
SO   PCT Int. Appl., 147 pp.
     CODEN: PIXXD2
```

DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002004488	A2	20020117	WO 2001-GB3130	20010712

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 2000-614679 A 20000712

AB **Nucleic acid-binding polypeptides** are designed capable of **binding** to one or more of telomeric, G-**quadruplex**, or G-quartet **nucleic acid** as an inhibitor of enzymic activity, including a telomerase activity, a polymerase activity, an integrase activity, and a gp120 activity. Gq1 is an artificial **protein** that has been engineered from **zinc finger** motifs to bind human telomeric G-**quadruplex** **DNA**. Primer extension studies using both telomerase and Klenow fragment of Escherichia coli **DNA** polymerase I suggest that Gq1 can inhibit both the synthesis and copying of telomeric **DNA** sequences. Since this **zinc finger protein** has no detectable affinity for telomeric duplex **DNA**, Gq1 may prove an attractive probe for carrying out cell-based studies. Telomerase assays as well as methods of identifying mols. capable of interacting with telomeric, G-**quadruplex**, or G-quartet **nucleic acid** are described. A stable integrated Gq1 **zinc finger** repressor is shown to inhibit HIV-1 replication in human T-cells.

IT **390883-06-4P 390883-09-7P 390883-11-1P**
390883-13-3P 390883-15-5P
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; encoding **zinc finger** synthetic **polypeptides binding** to telomeric G **quadruplex DNA**)

IT **390883-30-4**
RL: PRP (Properties)
(unclaimed sequence; **zinc finger** synthetic **polypeptides binding** to telomeric G **quadruplex DNA**)

L57 ANSWER 2 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 2001:408061 HCAPLUS
DN 135:30537
TI Design, construction and of **zinc finger** protein derivatives and their use in the modulation of gene expression
IN Barbas, Carlos F., III; Gottesfeld, Joel M.; Wright, Peter E.
PA The Scripps Research Institute, USA
SO U.S., 67 pp., Cont.-in-part of U.S. Ser. No. 312,604, abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6242568	B1	20010605	US 1996-676318	19961230 <--
WO 9519431	A1	19950720	WO 1995-US829	19950118 <--

W: AU, CA, FI, JP, NO, US

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRAI US 1994-183119 B2 19940118 <--
US 1994-312604 B2 19940928 <--
WO 1995-US829 W 19950118 <--

AB The present invention provides **zinc finger** nucleotide binding protein variants that have at least two **zinc finger** modules that bind to a target cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence. Also provided are methods of use of such **zinc finger** nucleotide binding protein variants and methods for isolating the same using expression libraries encoding the protein variants contg. randomized substitutions of amino acids. Exemplary **zinc finger** nucleotide binding protein variants of the invention include two cysteines and two histidines whereby both cysteines are amino proximal to both histidines. Design and construction of variants of the **zinc finger** protein Zif/268 are disclosed. Construction of multifinger proteins utilizing repeats of the first **finger** of Zif/268 is described.

IT **343429-13-0P**
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BPR (Biological process); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process)
(amino acid sequence; design, construction and of **zinc finger** protein derivs. and their use in modulation of gene expression)

IT **169108-70-7P 169108-73-0P 169108-74-1P 169108-76-3P**
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BPR (Biological process); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process)
(design, construction and of **zinc finger** protein derivs. and their use in modulation of gene expression)

IT **343581-44-2**
RL: PRP (Properties)
(unclaimed protein sequence; design, construction and of **zinc finger** protein derivs. and their use in the modulation of gene expression)

IT **343321-37-9**
RL: PRP (Properties)
(unclaimed sequence; design, construction and of **zinc finger** protein derivs. and their use in the modulation of gene expression)

IT **168971-84-4**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(**zinc finger** linker peptide; design, construction and of **zinc finger** protein derivs. and their use in modulation of gene expression)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Agarwal, K	1991	30	7842	Biochemistry	HCAPLUS
Barbas, C	1992	89	4457	Proceedings of the N	HCAPLUS
Bergqvist, A	1990	18	2715	Nucleic Acids Resear	HCAPLUS
Call	1994			US 5350840	HCAPLUS
Celenza, J	1986	233	1175	Science	HCAPLUS
de The	1994			US 5376530	HCAPLUS
Debs, R	1990	265	10189	The Journal of Biolo	HCAPLUS
Evans	1997			US 5597693	HCAPLUS
Fernandez-Pol	1993			US 5243041	HCAPLUS
Jacobs, G	1992	11	4507	The EMBO Journal	HCAPLUS
Jamieson, A	1994	33	5689	Biochemistry	HCAPLUS
Julian, N	1993	331	43	FEBS Letters	HCAPLUS
Katagiri	1991			US 4990607	HCAPLUS
Ladner	1992			US 5096815	HCAPLUS

Ladner	1995			US 5403484	HCAPLUS
Nabel	1994			US 5324818	HCAPLUS
Pabo, C	1992	61	1053	Annual Review of Bio	HCAPLUS
Quigley, C	1992	6	1103	Molecular Endocrinol	HCAPLUS
Rauscher, F	1990	250	1259	Science	HCAPLUS
Ray, A	1991	88	7086	Proceedings of the N	HCAPLUS
Rollins, M	1993	13	4776	Molecular and Cellul	HCAPLUS
Singh, H	1988	52	415	Cell	HCAPLUS
South, T	1990	29	7786	Biochemistry	HCAPLUS
Stevens	1994			US 5340739	HCAPLUS
Tao	1994			US 5324638	HCAPLUS
Thukral, S	1992	12	2784	Molecular and Cellul	MEDLINE
Wright, J	1990	248	588	Science	HCAPLUS
Yu, M	1993	90	6340	Proceedings of the N	HCAPLUS

L57 ANSWER 3 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1999:686615 HCAPLUS
DN 131:308157
TI cDNA molecules encoding human and chicken CTCF (CCCTC-binding factor), sequences and uses thereof
IN Lobanenkov, Victor L.; Neiman, Paul E.; Klenova, Elena M.; Goodwin, Graham H.; Filippova, Galina N.; Collins, Steven J.; Nicolas, Robert H.
PA Fred Hutchinson Cancer Research Center, USA; Cancer Research Campaign Technology, Ltd.
SO U.S., 37 pp., Cont.-in-part of U.S. Ser. No. 261,680, abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 5972643	A	19991026	US 1995-475844	19950607 <--
CA 2205203	AA	19951228	CA 1995-2205203	19950615 <--
PRAI US 1994-261680		19940617 <--		

AB This invention provides the isolation and purifn. of polynucleotides (genomic **DNA**, cDNA, antisense RNA) encoding human and chicken CCCTC-**binding** factor (CTCF). CTCF is a sequence-specific **DNA binding protein** that contains eleven **zinc finger binding** domains and is capable of **binding** to the 5'-flanking region of the c-myc gene. The invention also provides methods for producing recombinant CTCF by inserting **nucleic acid** mols. encoding CTCF into a suitable expression vector and use of said expression vector to transform prokaryotic or eukaryotic cells. The cDNA and amino acid sequences of chicken and human CTCF are provided. Using Northern blot anal. the invention revealed four major chicken CTCF gene mRNA species, indicating that the CTCF gene may encode multiple **proteins** by generating a variety of mRNA isoforms. The invention further showed that CTCF acts as a repressor of the human c-myc gene P2 promoter. The invention also discussed the potential use of CTCF **polypeptides** and antibodies to identify mutant CTCFs in methods of diagnosis.

IT **152890-29-4P 177404-57-8P**
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BPR (Biological process); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process)
(amino acid sequence; human and chicken CTCF (CCCTC-binding factor), cDNA and amino acid sequences, recombinant prodn. and binding to gene c-myc 5'-flanking region)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Arnold	1996	24	2640	Nucleic Acids Resear	HCAPLUS
Askew	1991	6	1915	Oncogene	HCAPLUS
Basu	1993	268	4188	J Biol Chem	HCAPLUS
Ben-David	1991	66	831	Cell	MEDLINE

Ben-David	1990	87	1332	Proc Natl Acad Sci U	HCAPLUS
Berg	1990	265	6513	J Biol Chem	HCAPLUS
Beug	1982	1	195	J Cell Physiol Suppl	MEDLINE
Bickmore	1992	257	235	Science	HCAPLUS
Bird	1986	321	209	Nature	HCAPLUS
Blackwood	1991	251	1211	Science	HCAPLUS
Bossone	1992	89	7452	Proc Natl Acad Sci U	HCAPLUS
Burcin	1994	5	337	Cancer Biology	HCAPLUS
Carter	1990	87	8751	Proc Natl Acad Sci U	MEDLINE
Cole	1986	20	361	Annu Rev Genet	HCAPLUS
El-Baradi	1991	35	155	Mech Devel	HCAPLUS
Flanagan	1992	12	38	Mol Cell Biol	MEDLINE
Franklin	1994	14	6773	Mol Cell Biol	HCAPLUS
Fried	1981	9	6505	Nuc Acids Res	HCAPLUS
Gould	1989	86	1934	Proc Natl Acad Sci U	HCAPLUS
Helin	1992	70	337	Cell	HCAPLUS
Hsu	1992	257	1946	Science	HCAPLUS
Jacobs	1985	313	806	Nature	HCAPLUS
Kadonaga	1991	208	10	Methods Enzymol	HCAPLUS
Kadonaga	1988	242	1566	Science	HCAPLUS
Kim	1990	10	3224	Mol Cell Biol	HCAPLUS
Kingsley	1992	12	4251	Mol Cell Biol	HCAPLUS
Klenova	1993	13	7612	Mol Cell Biol	HCAPLUS
Kohlhuber	1993	8	1099	Oncogene	HCAPLUS
Kohne	1993	232	747	J Mol Biol	MEDLINE
Kolluri	1991	17	4771	Nucl Acids Res	
Kretzner	1992	359	426	Nature	HCAPLUS
Krumm	1992	6	2201	Genes 7 Devel	HCAPLUS
Lathe	1985	183	1	J Mol Biol	HCAPLUS
Lobanenkov	1986	159	181	Eur J Biochem	HCAPLUS
Lobanenkov	1989		45	Gene Reg and AIDS	
Lobanenkov	1990	5	1743	Oncogene	HCAPLUS
Marcu	1992	61	809	Annual Rev Biochem	HCAPLUS
Matsudaira	1987	262	10035	J Biol Chem	HCAPLUS
Mattes	1992			US 5143843	HCAPLUS
Morishita	1992	89	3937	Proc Natl Acad Sci U	HCAPLUS
Neiman	1991	88	5857	Proc Nal Acad Sci US	MEDLINE
Ngo	1994		433	The Protein Folding	HCAPLUS
Nicolas	1993		81	Transcription Factor	HCAPLUS
Pyrc	1992	31	4102	Biochem	HCAPLUS
Ray	1991	11	2154	Mol Cell Biol	HCAPLUS
Riggs	1993	13	7487	Mol Cell Biol	HCAPLUS
Roy	1991	354	245	Nature	HCAPLUS
Sambrook	1989		8.2	Molecular Cloning: A	
Sen	1986	46	705	Cell	HCAPLUS
Shih	1984	81	4697	Proc Natl Acad Sci U	HCAPLUS
Smulson	1993			US 5272057	HCAPLUS
Spencer	1991	56	1	Adv Cancer REs	HCAPLUS
St-Arnaud	1993	13	1590	Mol Cell Biol	HCAPLUS
Stappert	1992	20	624	Nucl Acids Res	HCAPLUS
Stobl	1992	11	3307	EMBO J	
Tevosian	1991	25	1013	Molecul Biol (Moscow	MEDLINE
Tsuda	1990	87	6791	Proc Natl Acad Sci U	HCAPLUS
van Lohuizen	1990	1032	213	Biochimica et Biophy	HCAPLUS

L57 ANSWER 4 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1999:614102 HCAPLUS
DN 131:238849
TI A **DNA-binding zinc finger protein** specific for a modified base-containing sequence
IN **Choo, Yen; Isalan, Mark**
PA Medical Research Council, UK
SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9947656	A2	19990923	WO 1999-GB816	19990317 <--
	WO 9947656	A3	19991125		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

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	EP 1064369	A2	20010103	EP 1999-910512	19990317 <--

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

	JP 2002506640	T2	20020305	JP 2000-536839	19990317 <--
PRAI	GB 1998-5576	A	19980317	<--	
	GB 1998-6895	A	19980331	<--	
	GB 1998-7246	A	19980403	<--	
	WO 1999-GB816	W	19990317		

AB A modified **Cys2-His2 zinc finger** that binds to a target nucleic acid sequence contg. a modified base but not to an identical sequence contg. an equiv. unmodified base is described. The **zinc finger** can be used to create sequence-specific reagents, such as restriction enzymes with novel sequence requirements or for the assay of DNA methylation. **Zinc fingers** capable of binding 5-Me cytosine-contg. DNA were derived from one of the **fingers** of Zif268 (Egr-1) by several rounds of screening of a phage display library using increasing stringency of selectivity of binding to screen for sequence-specific, selective binding. Rules relating the amino acid sequence of a **zinc finger** to its DNA binding specificity are also outlined. **Zinc fingers** showing up to a 31-fold difference in dissocn. consts. of <100 nM for binding with 5-Me cytosine-contg. DNA and its cytosine-contg. analog were obtained.

IT **133551-05-0 216434-95-6**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(methylated **DNA binding zinc finger; DNA-binding zinc finger protein** specific for modified base-contg. sequence)

L57 ANSWER 5 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:790665 HCAPLUS
DN 130:35366
TI **Recognition code** for the design of synthetic **nucleic acid-binding proteins**
IN **Choo, Yen; Klug, Aaron; Isalan, Mark**
PA Medical Research Council, UK
SO PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9853060	A1	19981126	WO 1998-GB1516	19980526 <--

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

AU 9875426	A1	19981211	AU 1998-75426	19980526	<--
AU 732017	B2	20010412			
EP 983351	A1	20000308	EP 1998-922967	19980526	<--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI					
JP 2001527417	T2	20011225	JP 1998-550158	19980526	<--
PRAI GB 1997-10809	A	19970523	<--		
WO 1998-GB1516	W	19980526	<--		

OS MARPAT 130:35366

AB The invention provides a method for prepg. a **nucleic acid binding protein** of the **Cys2-His2 zinc finger** class capable of **binding** to a target **quadruplet nucleic acid** sequence. A more complete code is provided which permits the selection of any **nucleic acid** sequence as the target sequence, and the design of a specific **nucleic acid-binding protein** which will bind thereto. Moreover, the invention provides a method by which a **zinc finger protein** specific for any given **nucleic acid** sequence may be designed and optimized. If bas 4 in the **quadruplet** is A, then position +6 in the .**alpha**.-**helix** is Gln and position ++2 is not Asp; and if base 4 in the **quadruplet** is C, then position +6 in the .**alpha**.-**helix** may be any residue, as long as position ++2 in the . **alpha**.-**helix** is not Asp. The **recognition code** is used to design (1) a **protein** whereby the target is the activating point mutation in codon 12 of the human EJ bladder carcinoma Ha-ras oncogene (GGC.fwdarw.GTC), and (2) an anti-HIV **zinc finger binding** to the tat-specific sequence 5'-agagagctc-3'.

IT **216493-25-3P**
RL: BPN (Biosynthetic preparation); BPR (Biological process); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process)
(anti-HIV **zinc finger** designed for specific **nucleic acid binding; recognition code** for the design of synthetic **nucleic acid-binding proteins**)

IT **216434-95-6P**
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(model consensus **zinc finger; recognition code** for the design of synthetic **nucleic acid-binding proteins**)

IT **216434-99-0P 216435-00-6P 216435-01-7P 216437-56-8P 216437-57-9P 216437-58-0P 216437-59-1P 216437-60-4P 216437-61-5P 216582-15-9P 216583-28-7P**
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(**zinc finger** designed for **binding** to Ha-ras oncogene; **recognition code** for the design of synthetic **nucleic acid-binding proteins**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Choo, Y	1996			WO 9606166 A	HCAPLUS
Choo, Y	1997	7	117	Curr Op Struct Biol	HCAPLUS
Choo, Y	1994	91	11163	Proceedings of the N	HCAPLUS
Choo, Y	1994	91	11168	Proceedings of the N	HCAPLUS
Elrod-Erickson, M	1996	4	1171	Structure	HCAPLUS
Isalan, M	1997	94	5617	Proceedings of the N	HCAPLUS

L57 ANSWER 6 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:790664 HCAPLUS
DN 130:35365
TI **Recognition code** for the design of synthetic **nucleic acid-binding proteins**
IN **Choo, Yen; Klug, Aaron; Isalan, Mark**
PA Medical Research Council, UK
SO PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9853059	A1	19981126	WO 1998-GB1514	19980526 <--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9875424	A1	19981211	AU 1998-75424	19980526 <--
PRAI	GB 1997-10807		19970523 <--		
	WO 1998-GB1514		19980526 <--		

OS MARPAT 130:35365
AB The invention provides a method for prepg. a **nucleic acid binding protein** of the **Cys2-His2 zinc finger** class capable of **binding** to a target triplet **nucleic acid** sequence. A more complete code is provided which permits the selection of any **nucleic acid** sequence as the target sequence, and the design of a specific **nucleic acid-binding protein** which will bind thereto. Moreover, the invention provides a method by which a **zinc finger protein** specific for any given **nucleic acid** sequence may be designed and optimized. **Binding** to the 5' base of the triplet by an **.alpha.-helical zinc finger nucleic acid binding** motif in the **protein** is detd. as follows: if the 5' base in the triplet is A, then position +6 in the **.alpha.-helix** is Glu, Asn or Val; if the 5' base in the triplet is C, then position +6 in the **.alpha.-helix** is Ser, Thr, Val, Ala, Glu or Asn. The **recognition code** is used to design (1) a **protein** whereby the target is the activating point mutation in codon 12 of the human EJ bladder carcinoma Ha-ras oncogene (GGC.fwdarw.GTC), (2) an anti-HIV **zinc finger binding** to the tat-specific sequence 5'-agagagctc-3', and (3) design of a **zinc finger** specific for an 8-bp palindrome (gcggccgc).
IT **216493-25-3P**
RL: BPN (Biosynthetic preparation); BPR (Biological process); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process)
(anti-HIV **zinc finger** designed for specific **nucleic acid binding; recognition code** for the design of synthetic **nucleic acid -binding proteins**)
IT **216434-95-6P**
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(model consensus **zinc finger; recognition code** for the design of synthetic **nucleic acid -binding proteins**)
IT **216434-99-0P 216435-00-6P 216435-01-7P 216582-68-2P**

RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(**zinc finger** designed for **binding** to Ha-ras oncogene; **recognition code** for the design of synthetic **nucleic acid-binding proteins**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Choo, Y	1996			WO 9606166 A	HCAPLUS
Choo, Y	1997	7	117	Curr Op Struct Biol	HCAPLUS
Choo, Y	1994	91	11163	Proceedings of the N	HCAPLUS
Choo, Y	1994	91	11168	Proceedings of the N	HCAPLUS
Elrod-Erickson, M	1996	4	1171	Structure	HCAPLUS
Fairall, L	1993	366	483	Nature	HCAPLUS
Houbaviy, H	1996	93	13577	Proceedings of the N	HCAPLUS
Ikeda, M	1996	181	167	Gene	MEDLINE
Isalan, M	1997	94	5617	Proceedings of the N	HCAPLUS
Jamieson, A	1994	33	5689	Biochemistry	HCAPLUS
Pavletich, N	1993	261	1701	Science	HCAPLUS
Suzuki, M	1994	91	12357	Proceedings of the N	HCAPLUS
Wu, H	1995	92	344	Proc Natl Acad Sci	HCAPLUS

L57 ANSWER 7 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:790663 HCAPLUS
DN 130:35364
TI **Recognition code** for the design of synthetic **nucleic acid-binding proteins**
IN **Choo, Yen; Klug, Aaron; Isalan, Mark**
PA Medical Research Council, UK
SO PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9853058	A1	19981126	WO 1998-GB1512	19980526 <--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9875423	A1	19981211	AU 1998-75423	19980526 <--
	EP 983350	A1	20000308	EP 1998-922964	19980526 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI	GB 1997-10809	A	19970523 <--		
	WO 1998-GB1512	W	19980526 <--		

OS MARPAT 130:35364
AB The invention provides a method for prepg. a **nucleic acid binding protein** of the **Cys2-His2 zinc finger** class capable of **binding** to a target **quadruplet nucleic acid** sequence. **Zinc finger binding** sites are detd. by overlapping 4-bp subsites, and sequence specificity at the boundary between subsites arises from synergy between adjacent **finger**.s. A more complete code is provided which permits the selection of any **nucleic acid** sequence as the target sequence, and the design of a specific **nucleic acid-binding protein** which will bind thereto. Moreover, the invention provides a method by which a **zinc finger**

protein specific for any given **nucleic acid** sequence may be designed and optimized. **Binding** to base 4 of the **quadruplet** by an **.alpha.-helical zinc finger nucleic acid-binding** motif in the **protein** is detd. as follows: if base 4 in the **quadruplet** is A, then position +6 in the **.alpha.-helix** is Glu, Asn, or Val; if base 4 in the **quadruplet** is C, then position +6 in the **.alpha.-helix** is Ser, Thr, Val, Ala, Glu, or Asn. The **recognition code** is used to design (1) a **protein** whereby the target is the activating point mutation in codon 12 of the human EJ bladder carcinoma Ha-ras oncogene (GGC.fwdarw.GTC), (2) an anti-HIV **zinc finger binding** to the tat-specific sequence 5'-agagagctc-3', and (3) design of a **zinc finger** specific for an 8-bp palindrome (gcggccgc).

IT **216493-25-3P**
RL: BPN (Biosynthetic preparation); BPR (Biological process); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process)
(anti-HIV **zinc finger** designed for specific **nucleic acid binding; recognition code** for the design of synthetic **nucleic acid -binding proteins**)

IT **216434-95-6P**
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(model consensus **zinc finger; recognition code** for the design of synthetic **nucleic acid -binding proteins**)

IT **216434-99-0P 216435-00-6P 216435-01-7P 216582-68-2P**
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(**zinc finger** designed for **binding** to Ha-ras oncogene; **recognition code** for the design of synthetic **nucleic acid-binding proteins**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Choo, Y	1996			WO 9606166 A	HCAPLUS
Isalan, M	1997	94	5617	Proceedings of the N	HCAPLUS

L57 ANSWER 8 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:786691 HCAPLUS
DN 130:149362
TI Isolation and functional characterization of cDNA of serum amyloid A-activating factor that binds to the serum amyloid A promoter
AU Ray, Alpana; Ray, Bimal K.
CS Department of Veterinary Pathobiology, University of Missouri, Columbia, MO, 65211, USA
SO Mol. Cell. Biol. (**1998**), 18(12), 7327-7335
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB Serum amyloid A (SAA), a plasma **protein** inducible in response to many inflammatory conditions, is assocd. with the pathogenesis of several diseases including reactive amyloidosis, rheumatoid arthritis, and atherosclerosis. The authors have previously reported an element of the SAA promoter, designated SAA-activating sequence (SAS), that is involved in the inflammation-induced SAA expression, and a nuclear factor, SAS-**binding** factor (SAF), that interacts with the SAS element has been identified previously (A. Ray and B. K. Ray, Mol. Cell. Biol. 16:1584-1594, 1996). To evaluate how SAF is involved in SAA promoter activation, the authors have investigated structural features and

functional characteristics of this transcription factor. These studies indicate that SAF belongs to a family of transcription factors characterized by the presence of multiple **zinc finger** motifs of the **Cys2-His2** type at the carboxyl end. Of the three cloned SAF cDNAs (SAF-1, SAF-5, and SAF-8), SAF-1 isoform showed a high degree of homol. to MAZ/ZF87/Pur-1 **protein** while SAF-5 and SAF-8 isoforms are unique and are related to SAF-1/MAZ/ZF87/Pur-1 at the **zinc finger** domains but different elsewhere. Although structurally distinct, all members are capable of activating SAS element-mediated expression and display virtually identical sequence specificities. However, varying levels of expression of members of this gene family were obsd. in different tissues. Functional activity of SAF is regulated by a posttranslational event as SAF **DNA-binding** and transactivation abilities are increased by a **protein** phosphatase inhibitor, okadaic acid, and inhibited by a **protein** kinase inhibitor, H7. Consistent with this observation, increased **DNA binding** of the cloned SAF and its hyper-phosphorylation, in response to okadaic acid treatment of the transfected cells, were obsd. Taken together, our results suggest that, in addn. to tissue-specific expression, SAFs, a family of **zinc finger** transcription factors, undergo a modification by a posttranslational event that confers their SAA promoter-**binding** activity and transactivation potential.

IT **220202-75-5 220202-76-6 220202-78-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; isolation and functional characterization of cDNA of serum amyloid A-activating factor that binds to serum amyloid promoter)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Alexandropoulos, K	1995	92	3110	Proc Natl Acad Sci U	HCAPLUS
Alvarez, E	1991	266	15277	J Biol Chem	HCAPLUS
Baeuerle, P	1988	53	211	Cell	HCAPLUS
Benson, M	1979	22	36	Arthritis Rheum	MEDLINE
Betts, J	1993	268	25624	J Biol Chem	HCAPLUS
Bossone, S	1992	89	7452	Proc Natl Acad Sci U	HCAPLUS
Bradford, M	1976	72	248	Anal Biochem	HCAPLUS
Call, K	1990	60	509	Cell	HCAPLUS
Chang, C	1990		273	Structure and functi	
Chomczynski, P	1987	162	156	Anal Biochem	HCAPLUS
Cobb, M	1991	2	965	Cell Regul	HCAPLUS
Coetzee, G	1986	261	9644	J Biol Chem	HCAPLUS
Duncan, D	1995	15	3179	Mol Cell Biol	MEDLINE
Edbrooke, M	1989	9	1908	Mol Cell Biol	HCAPLUS
Graham, F	1973	52	456	Virology	MEDLINE
Huang, J	1994	14	4475	Mol Cell Biol	HCAPLUS
Kania, M	1990	4	1701	Genes Dev	HCAPLUS
Kennedy, G	1992	89	11498	Proc Natl Acad Sci U	HCAPLUS
Koleske, A	1992	69	883	Cell	HCAPLUS
Kunz, D	1989	17	1121	Nucleic Acids Res	HCAPLUS
Kushner, I	1982	389	39	Ann N Y Acad Sci	HCAPLUS
Li, X	1991	266	15192	J Biol Chem	HCAPLUS
Long, G	1984	23	4828	Biochemistry	HCAPLUS
Lowell, C	1986	261	8453	J Biol Chem	HCAPLUS
Luckow, B	1987	15	5490	Nucleic Acids Res	HCAPLUS
Macdonald, P	1986	47	721	Cell	HCAPLUS
Malle, E	1993	102	131	Atherosclerosis	HCAPLUS
Mermod, N	1989	58	741	Cell	HCAPLUS
Mitchell, P	1989	245	371	Science	HCAPLUS
Parks, C	1996	271	4417	J Biol Chem	HCAPLUS
Poole, S	1985	40	37	Cell	HCAPLUS
Pyrc, J	1992	31	4102	Biochemistry	HCAPLUS
Ray, A	1993	3	151	Gene Expr	HCAPLUS

Ray, A	1995	270	7365	J Biol Chem	HCAPLUS
Ray, A	1994	14	4324	Mol Cell Biol	HCAPLUS
Ray, A	1996	16	1584	Mol Cell Biol	HCAPLUS
Ray, B	1992	185	69	Biochem Biophys Res	HCAPLUS
Ray, B	1993	193	1159	Biochem Biophys Res	HCAPLUS
Ray, B	1997	36	4662	Biochemistry	HCAPLUS
Ray, B	1997	272	28948	J Biol Chem	HCAPLUS
Rossomando, A	1991	266	20270	J Biol Chem	HCAPLUS
Sambrook, J	1989			Molecular cloning:a	
Singh, H	1988	52	415	Cell	HCAPLUS
Sipe, J	1992	61	947	Annu Rev Biochem	HCAPLUS
Steinmetz, A	1989	1006	173	Biochim Biophys Acta	HCAPLUS
Sturgill, T	1991	1092	350	Biochim Biophys Acta	HCAPLUS
Wadzinski, B	1993	13	2822	Mol Cell Biol	HCAPLUS
Wegenka, U	1993	13	276	Mol Cell Biol	HCAPLUS
Williamson, M	1994	297	249	Biochem J	HCAPLUS
Wilson, D	1990	10	6181	Mol Cell Biol	HCAPLUS
Zhang, D	1996	271	9503	J Biol Chem	HCAPLUS

L57 ANSWER 9 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:704604 HCAPLUS
DN 130:61946
TI Cloning the cDNA for a new human **zinc finger** protein defines a group of closely related Kruppel-like transcription factors
AU Matsumoto, Nobukyuki; Laub, Friedrich; Aldabe, Rafael; Zhang, Wen; Ramirez, Francesco; Yoshida, Teruhiko; Terada, Masaaki
CS Genetics Division, National Cancer Center Research Institute, Tokyo, 104-0045, Japan
SO J. Biol. Chem. (**1998**), 273(43), 28229-28237
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB We have identified a novel **zinc finger protein** that has been named ubiquitous Kruppel-like factor (UKLF) based on structural considerations and the pattern of gene expression. UKLF was isolated by the polymerase chain reaction approach using degenerate oligonucleotides corresponding to the **DNA-binding** domain of erythroid Kruppel-like factor (EKLF) and cDNA prepd. from human vascular endothelial cells. The carboxyl-terminal portion of UKLF contains three **zinc fingers** of the **Cys2-His2** type and binds in vitro to the CACCC motif of the .beta.-globin promoter and to the Sp1 **recognition** sequence. The amino-terminal portion of UKLF consists of a hydrophobic region rich in serines and a neg. charged segment with several glutamic acid residues. The first 47 amino acids of the acidic region are nearly identical to the amino-terminal portion of another Kruppel-like factor, the so-called core promoter-**binding protein** (CPBP) or Zf9. Like CPBP/Zf9, UKLF can function as a transcription activator in co-transfection assays. However, this activity is lost when the highly conserved amino-terminal segment is deleted. These findings indicate that UKLF and CPBP/Zf9 represent a distinct subgroup of closely related Kruppel-like activators of transcription. Mapping of the UKLF gene to chromosome 2 suggested that UKLF and CPBP/Zf9 translocated to different chromosomes following duplication from an ancestral gene.
IT **217798-42-0**
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)
(amino acid sequence; cloning the cDNA for a new human **zinc finger** protein defines a group of closely related Kruppel-like transcription factors)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Anderson, K	1995	15	5957	Mol Cell Biol	HCAPLUS

Berg, J	1990	265	6513	J Biol Chem	HCAPLUS
Chen, X	1996	15	5888	EMBO J	HCAPLUS
Chomczynski, P	1987	162	156	Anal Biochem	HCAPLUS
Crossley, M	1996	16	1695	Mol Cell Biol	HCAPLUS
El Rouby, S	1996	13	2623	Oncogene	HCAPLUS
Friedman, S	1996	14	101	Prog Liver Dis	HCAPLUS
Garret-Sinha, L	1996	271	31384	J Biol Chem	
Gill, G	1987	51	121	Cell	HCAPLUS
Hahn, S	1993	72	481	Cell	HCAPLUS
Heng, H	1992	89	9509	Proc Natl Acad Sci U	HCAPLUS
Ide, H	1995	311	675	Biochem J	HCAPLUS
Inagaki, Y	1994	269	14828	J Biol Chem	HCAPLUS
Johnson, R	1991	87	847	J Clin Invest	HCAPLUS
Klevitt, R	1991	253	1367	Science	
Koritschoner, N	1996	236	365	Eur J Biochem	HCAPLUS
Koritschoner, N	1997	272	9573	J Biol Chem	HCAPLUS
Kuhn, C	1991	138	1257	Am J Pathol	MEDLINE
Kuo, C	1997	11	2996	Genes Dev	HCAPLUS
Kuo, C	1997	277	1986	Science	HCAPLUS
Lalazar, A	1997	195	235	Gene	HCAPLUS
Leuther, K	1993	72	575	Cell	HCAPLUS
Maruyama, I	1995	23	3796	Nucleic Acids Res	HCAPLUS
Miller, I	1993	13	2776	Mol Cell Biol	HCAPLUS
Miller, J	1995	4	1609	EMBO J	
Mitchell, P	1989	245	371	Science	HCAPLUS
Nuez, B	1995	375	316	Nature	HCAPLUS
Onyango, P	1998	48	143	Genomics	HCAPLUS
Perkins, A	1995	375	318	Nature	HCAPLUS
Ratzin, V	1998	95	9500	Proc Natl Acad Sci U	
Sambrook, J	1989			Molecular Cloning:A	
Schur, R	1986	47	1025	Cell	
Shields, J	1986	271	20009	J Biol Chem	
Shields, J	1988	272	18504	J Biol Chem	
Shields, J	1998	26	796	Nucleic Acids Res	HCAPLUS
Sogo, K	1993	21	1527	Nucleic Acids Res	
Watanabe, T	1998	18	442	Mol Cell Biol	HCAPLUS
Yet, S	1998	273	1026	J Biol Chem	HCAPLUS

L57 ANSWER 10 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:294709 HCAPLUS
DN 129:145538
TI Helios, a T cell-restricted Ikaros family member that quantitatively associates with Ikaros at centromeric heterochromatin. [Erratum to document cited in CA129:23889]
AU Hahm, Kyungmin; Cobb, Bradley S.; McCarty, Aaron S.; Brown, Karen E.; Klug, Christopher A.; Lee, Robert; Akashi, Koichi; Weissman, Irving L.; Fisher, Amanda G.; Smale, Stephen T.
CS Howard Hughes Medical Institute, Molecular Biology Institute, and Department of Microbiology and Immunology, UCLA School of Medicine, Los Angeles, CA, 90095-1662, USA
SO Genes Dev. (**1998**), 12(8), 1240
CODEN: GEDEEP; ISSN: 0890-9369
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The name of Irving L. Weissman was spelled incorrectly in the Table of Contents of this issue.
IT **207870-86-8**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence of limiting regulatory subunit of Ikaros; cdna sequence of mouse helios T cell-restricted Ikaros family member that quant. assocs. with Ikaros at centromeric heterochromatin (Erratum))

L57 ANSWER 11 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:289907 HCAPLUS

DN 129:23889
TI Helios, a T cell-restricted Ikaros family member that quantitatively associates with Ikaros at centromeric heterochromatin
AU Hahm, Kyungmin; Cobb, Bradley S.; McCarty, Aaron S.; Brown, Karen E.; Klug, Christopher A.; Lee, Robert; Akashi, Koichi; Weissman, Irving L.; Fisher, Amanda G.; Smale, Stephen T.
CS Howard Hughes Medical Institute, Molecular Biology Institute, and Department of Microbiology and Immunology, UCLA School of Medicine, Los Angeles, CA, 90095-1662, USA
SO Genes Dev. (**1998**), 12(6), 782-796
CODEN: GEDEEP; ISSN: 0890-9369
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The Ikaros gene encodes multiple protein isoforms that contribute crit. functions during the development of lymphocytes and other hematopoietic cell types. The intracellular functions of Ikaros are not known, although recent studies have shown that Ikaros proteins colocalize with inactive genes and centromeric heterochromatin. In this study, Ikaros proteins were found to be components of highly stable complexes. The complexes from an immature T cell line were purified, revealing assocd. proteins of 70 and 30 kD. The p70 gene, named Helios, encodes two protein isoforms with **zinc finger** domains exhibiting considerable homol. to those within Ikaros proteins. Helios and Ikaros **recognize** similar DNA sequences and, when overexpressed, Helios assocs. indiscriminately with the various Ikaros isoforms. Although Ikaros is present in most hematopoietic cells, Helios was found primarily in T cells. The relevance of the Ikaros-Helios interaction in T cells is supported by the quant. assocn. of Helios with a fraction of the Ikaros. Interestingly, the Ikaros-Helios complexes localize to the centromeric regions of T cell nuclei, similar to the Ikaros localization previously obsd. in B cells. Unlike the B cell results, however, only a fraction of the Ikaros, presumably the fraction assocd. with Helios, exhibited centromeric localization in T cells. These results establish immunoaffinity chromatog. as a useful method for identifying Ikaros partners and suggest that Helios is a limiting regulatory subunit for Ikaros within centromeric heterochromatin.
IT **207870-86-8**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(DNA-binding, amino acid sequence of limiting regulatory subunit of Ikaros; cdna sequence of mouse helios T cell-restricted Ikaros family member that quant. assocs. with Ikaros at centromeric heterochromatin)

L57 ANSWER 12 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1998:78103 HCAPLUS
DN 128:227538
TI End effects in DNA **recognition** by **zinc finger** arrays
AU **Choo, Yen**
CS Medical Research Council Laboratory of Molecular Biology, Cambridge, CB2 2QH, UK
SO Nucleic Acids Res. (**1998**), 26(2), 554-557
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The paradigmatic **DNA binding** domain from the transcription factor Zif268 contains three **zinc finger** modules in tandem repeat. When bound to their cognate **DNA** site the **fingers** read out the sequence of one **DNA** strand by making a linear series of successive base contacts. It is shown that the base-specific **protein-DNA** contacts made from the ends of the Zif268 three-**finger** array contribute less to the stability of the intermol. complex than do structurally equiv. contacts from more central regions of the **DNA binding** domain.

The effect is akin to the end fraying obsd. in duplex **nucleic acid** mols.

IT **204594-56-9**
RL: PEP (Physical, engineering or chemical process); PROC (Process)
(amino acid sequence; end effects in DNA **recognition** by **zinc finger** arrays)

L57 ANSWER 13 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1997:698566 HCAPLUS
DN 128:30912
TI Solution structure of the first three **zinc fingers** of TFIIIA bound to the cognate DNA sequence: determinants of affinity and sequence specificity
AU Wuttke, Deborah S.; Foster, Mark P.; Case, David A.; Gottesfeld, Joel M.; Wright, Peter E.
CS Department of Molecular Biology and the Skaggs Institute for Chemical Biology, La Jolla, CA, 92037, USA
SO J. Mol. Biol. (**1997**), 273(1), 183-206
CODEN: JMOBAK; ISSN: 0022-2836
PB Academic
DT Journal
LA English
AB The high resoln. soln. structure of a **protein** contg. the 3 N-terminal **zinc fingers** of Xenopus laevis transcription factor IIIA (TFIIIA) bound to its cognate **DNA** duplex was detd. by NMR spectroscopy. The **protein**, which is designated zf1-3, binds with all 3 **fingers** in the **DNA** major groove, with a no. of amino acids making base-specific contacts. The **DNA** structure is close to B-form. Although the mode of interaction of zf1-3 with **DNA** is similar to that of zif268 and other structurally characterized **zinc finger** complexes, the TFIIIA complex exhibits several novel features. Each **zinc finger** contacts 4-5 base-pairs and the repertoire of known base contact residues is extended to include a tryptophan at position +2 of the helix (**finger** 1) and arginine at position +10 (**finger** 3). Sequence-specific base contacts are made over virtually the entire length of the **finger** 3 helix. Lysine and histidine side-chains involved in base **recognition** are dynamically disordered in the soln. structure; in the case of lysine, in particular, this could significantly decrease the entropic cost of **DNA binding**. The **TGEKP**(N) linker sequences, which are highly flexible in the unbound **protein**, adopt ordered conformations on **DNA binding**. The linkers appear to play an active structural role in stabilization of the **protein-DNA** complex. Substantial **protein-protein** contact surfaces are formed between adjacent **fingers**. As a consequence of these **protein-protein** interactions, the orientation of **finger** 1 in the major groove differs from that of the other **fingers**. Contributions to high affinity **binding** by zf1-3 come from both direct **protein-DNA** contacts and from indirect **protein-protein** interactions assocd. with structural organization of the linkers and formation of well-packed interfaces between adjacent **zinc fingers** in the **DNA** complex. The structures provide a mol. level explanation for the large body of footprinting and mutagenesis data available for the TFIIIA-**DNA** complex.

IT **159575-54-9**
RL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)
(soln. structure of the first three **zinc fingers** of TFIIIA bound to the cognate DNA sequence and determinants of affinity and sequence specificity)

L57 ANSWER 14 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1997:643827 HCAPLUS
DN 127:327914

TI Synthesis and **DNA-binding** ability of Sp1 **protein zinc finger** domain and its peptidomimetics
AU Wang, Rui; Ni, Jingman; Hu, Xiaoyu; Ma, Yaping; Li, Xiangqun; Yang, Dingjian; Dong, Shouliang; Yang, Xiaowu; Pan, Xinfu
CS State Key Lab. Applied Organic Che,., Lanzhou Univ., Lanzhou, 730000, Peop. Rep. China
SO Sci. China, Ser. C: Life Sci. (**1997**), 40(5), 518-523
CODEN: SCCLFO; ISSN: 1006-9305
PB Science in China Press
DT Journal
LA English
AB The second **zinc finger** fragment of Sp1 (Sp1-ZF2), its mutant (Sp1-ZF2/HT. E20.fwdarw.H, R23.fwdarw.T), and two mimic analogs (ZF20 and ZF15) were synthesized by stepwise solid phase technique. The CD spectra and UV-visible spectrum with CoCl2 indicated that the formation of **zinc finger** structure was affected not only by the hydrophobic amino acids but also by the change of the distance between Cys and His. Gel-retardation electrophoresis assays indicated that the Glu and Arg residues are very important for **recognition**. A single **zinc finger** like Sp1-ZF2 is able to bind DNA sequence specifically.
IT **197923-45-8P 197923-46-9P**
RL: BAC (Biological activity or effector, except adverse); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(synthesis and **DNA-binding** ability of Sp1 **protein zinc finger** domain and peptidomimetics)

L57 ANSWER 15 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1997:245950 HCAPLUS
DN 126:302855
TI A novel human **zinc finger** protein that interacts with the core promoter element of a TATA box-less gene
AU Koritschoner, Nicolas P.; Bocco, Jose L.; Panzetta-Dutari, Graciela M.; Dumur, Catherine I.; Flury, Alfredo; Patrito, Luis C.
CS Departmento de Bioquimica Clinica, Facultad de Ciencias Quimicas, Universidad Nacional de Cordoba, Cordoba, Argent.
SO J. Biol. Chem. (**1997**), 272(14), 9573-9580
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The authors describe a novel human cDNA isolated by target site screening of a placental expression library, using as a probe, an essential element of a TATA box-less promoter corresponding to a pregnancy-specific glycoprotein gene. The cDNA encoded a predicted **protein** of 290 amino acids, designated core promoter-**binding protein** (CPBP), which has three **zinc fingers** (type **Cys2-His2**) at the end of its C-terminal domain, a serine/threonine-rich central region and an acidic domain lying within the N-terminal region. Addnl. sequence anal. and data base searches revealed that only the **zinc finger** domains are conserved (60-80% identity) in other transcription factors. In cotransfection assays, CPBP increased the transcription from a minimal promoter contg. its natural **DNA-binding** site. Moreover, a chimeric **protein** between CPBP and Gal4 **DNA binding** domain also increased the activity of an heterologous reporter gene contg. Gal4 **DNA binding** sites. The tissue distribution anal. of CPBP mRNA revealed that it is differentially expressed with an apparent enrichment in placental cells. The **DNA binding** and transcriptional activity of CPBP, in conjunction with its expression pattern, strongly suggests that this **protein** may participate in the regulation and/or maintenance of the basal expression of PSG and possibly other TATA box-less genes.
IT **189284-91-1**

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; cDNA sequence of a novel human **zinc finger** protein that interacts with the core promoter element of a TATA box-less gene)

L57 ANSWER 16 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1997:103680 HCAPLUS
DN 126:182011
TI Identification of amdX, a new **Cys-2-His-2** (C2H2) **zinc-finger** gene involved in the regulation of the amdS gene of Aspergillus nidulans
AU Murphy, Rachael L.; Andrianopoulos, Alex; Davis, Meryl A.; Hynes, Michael J.
CS Department of Genetics, The University of Melbourne, Parkville, 3052, Australia
SO Mol. Microbiol. (**1997**), 23(3), 591-602
CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell
DT Journal
LA English
AB The acetamidase-encoding amdS gene of Aspergillus nidulans has been shown to be controlled by multiple regulatory genes. A new gene, amdX, involved in amdS regulation was identified during the characterization of a translocation affecting amdS control. The amdX gene is predicted to encode a 1150-amino-acid poly-**peptide** which contains two **Cys-2-His-2** (C2H2) **zinc finger DNA-binding** motifs. Insertional inactivation of amdX and the phenotypes of transformants contg. multiple copies of the amdX gene show that it is an activator of amdS expression. A fusion **protein** contg. the AmdX **zinc fingers** was found to bind to sequences in the 5' region of amdS which overlap **binding** sites for the CreA and AmdA regulatory **proteins**. Evidence is presented for AmdX acting at these sites in vivo.
IT **187414-36-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; identification of amdX, a new **Cys-2-His-2** (C2H2) **zinc-finger** gene involved in regulation of amdS gene of Aspergillus nidulans)

L57 ANSWER 17 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1996:424019 HCAPLUS
DN 125:134177
TI A **zinc finger** gene from Onchocerca volvulus encodes a protein with a functional signal peptide and an unusual Ser-His **finger** motif
AU Holst, Corinna; Zipfel, Peter F.
CS Dep. Molecular Biol., Bernhard Nocht Inst. for Tropical Medicine, Hamburg, 20359, Germany
SO J. Biol. Chem. (**1996**), 271(28), 16725-16733
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The filarial parasite Onchocerca volvulus is the causative agent of river blindness. In order to identify genes potentially involved in parasite development we cloned a **zinc finger**-encoding gene from this species. The ovzf-1 gene represents one member of a family of related **zinc finger** genes. The predicted ovzf-1 translation product of 447 amino acids includes a hydrophobic signal peptide, which is followed by 13 contiguous **finger** motifs. The domains of **fingers** II-XIII display several conserved amino acids and a typical Krueppel-like **Cys2-His2** motif. The first **finger** domain has the two conserved Cys residues replaced with Ser residues; however, it includes all addnl. amino acids typical of

zinc finger domains. The N-terminal domain functions as a signal peptide, as it directs secretion of a reporter protein and a truncated Ovzf protein. Expression of an Ovzf protein via the secretory pathway was also confirmed by demonstrating attachment of N-linked carbohydrates to the recombinant protein. Although the recombinant Ovzf protein also includes a signal peptide, immunofluorescence analyses localize it inside a specific compartment of the infected insect cell. Expression of ovzf mRNA is developmentally regulated; no specific transcript is detected in adult female worms but in the infective L3. Identification of a secreted protein that might function in modulating gene expression of host cells provides an interesting tool for the study of parasite-host interaction on a biochem. and mol. level.

IT **180033-42-5**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; comparison of Onchocerca volvulus ovzf-1 and ovzf-2 gene products)

IT **180033-43-6**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; isolation and characterization of **zinc-finger** encoding gene ovzf-1 in Onchocerca volvulus)

L57 ANSWER 18 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1996:419878 HCAPLUS
DN 125:106854
TI A single amino acid determines the specificity for the target sequence of two **zinc-finger** proteins in plants
AU Takatsuji, Hiroshi
CS National Inst. Agrobiol. Resources, Tsukuba, 305, Japan
SO Biochem. Biophys. Res. Commun. (**1996**), 224(1), 219-223
CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA English
AB The EPF family is a group of **DNA-binding proteins** with two canonical **Cys2/His2 zinc-finger** motifs in Petunia. These **proteins** are unique in terms of structure in that (i) the two **zinc fingers** are sepd. by spacers of various lengths and (ii) the sequence QALGGH is strongly conserved in the **zinc-finger** motifs of members of the family. In this study, domain-swapping and site-directed mutagenesis expts. with two members of the **protein** family. EPF2-5 and EPF2-7, which have different target sequences, revealed that only a single amino acid in the second **zinc finger** is responsible for the difference in target specificity. The postion of this amino acid is different from those of determinants of target-sequence specificity in other **zinc-finger proteins**. Thus, the EPF family **recognizes** target sequences in a unique manner, together with the **recognition** of spacings in the target sequence that we demonstrated recently.

IT **179339-47-0**
RL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)
(second **zinc finger** of EPF2-5, **DNA binding** specificity of; single amino acid dets. specificity for target sequence of two **zinc-finger proteins** in plants)

L57 ANSWER 19 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1996:320586 HCAPLUS
DN 125:27275
TI A new **Cys2/His2 zinc finger** gene, rKr1, expressed in oligodendrocytes and neurons
AU Pott, Uwe; Colello, Raymond J.; Schwab, Martin E.
CS Brain Research Institute, University of Zurich, August Forel-Strasse 1, Zurich, CH-8029, Switz.

SO Mol. Brain Res. (**1996**), 38(1), 109-121
CODEN: MBREE4; ISSN: 0169-328X
DT Journal
LA English
AB The myelination of nerve fibers is essential for the function of the vertebrate nervous system as a prerequisite for fast saltatory conduction of action potentials. In the central nervous system (CNS), myelin is produced by oligodendrocytes. In order to identify gene regulatory **proteins** involved in the differentiation of this glial cell type or in the expression of myelin-specific genes, we have constructed a cDNA library from a highly enriched population of rat oligodendrocytes and screened this library for members of the Krueppel family of **Cys2 /His2 zinc finger proteins**. One of the identified clones, named rKr1, encodes a novel **protein** of 650 amino acids which contains 12 carboxy-terminal **zinc finger** domains and an amino-terminal acidic domain. On Northern blots, a single rKr1 mRNA of 4.3 kb is detected. This message is present in all adult rat tissues tested, with the highest levels found in the CNS and testis. In situ hybridization on the P15 brain revealed that the transcript is expressed in differentiated oligodendrocytes and in subtypes of neurons. Particularly high message levels are found in motor neurons of the brainstem and the spinal cord. The modular structure of the rKr1 **protein**, in which a potential **DNA binding** region (the **zinc fingers**) is combined with a putative activation domain (the acidic region), suggests a function as sequence-specific transcriptional activator.
IT **177773-66-9**
RL: PRP (Properties)
(amino acid sequence; **Cys2/His2 zinc finger** gene rKr1 expressed in oligodendrocytes and neurons)

L57 ANSWER 20 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1996:182634 HCAPLUS
DN 124:252560
TI Purification and characterization of the DNA-binding domain of BTEB, a GC box-binding transcription factor, expressed in Escherichia coli
AU Kikuchi, Yasuo; Sogawa, Kazuhiro; Watanabe, Nobuaki; Kobayashi, Akira; Fujii-Kuriyama, Yoshiaki
CS Dep. Chem., Graduate Sch. Sci., Tohoku Univ., Sendai, 980, Japan
SO J. Biochem. (Tokyo) (**1996**), 119(2), 309-13
CODEN: JOBIAO; ISSN: 0021-924X
DT Journal
LA English
AB BTEB is a GC-**binding protein** that regulates the transcription of genes with a single GC-box or tandemly repeated GC-boxes in the promoter. The **DNA-binding** domain of BTEB consists of 3 contiguous **Cys2-His2 zinc finger** motifs and short segments adjacent to their N- and C-terminal sides. The truncated BTEB (residues 120-244) contg. the **DNA-binding** domain was expressed in Escherichia coli and purified to homogeneity under denaturing conditions. **DNA-binding** activity of the BTEB was regenerated by refolding in the presence of Zn2+. The efficiency in regeneration was 70 .+-. 10%, and the dissocn. const. (Kd) of the **DNA**-complex was 4 .+-. 2 nM. Co2+ also regenerated the **DNA-binding** affinity of BTEB, albeit with less efficiency than Zn2+. Co-BTEB showed a slightly lower affinity to the specific **DNA** than **Zn**-BTEB. Refolding in the presence of Cd2+ resulted in an extremely low efficiency in regeneration of the **DNA-binding** activity. **Zn**-BTEB is in a monomer state at concns. <0.5 .mu.M, and forms a dimer in the concn. range of about 10-100 .mu.M.
IT **174883-39-7P**
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)
(amino acid sequence; purifn. and characterization of DNA-binding

domain of BTEB, a GC box-binding transcription factor, expressed in Escherichia coli)

L57 ANSWER 21 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1995:895545 HCAPLUS
DN 124:47002
TI A new **Cys2/His2 zinc finger** gene, rKr2, is expressed in differentiated rat oligodendrocytes and encodes a protein with a functional repressor domain
AU Pott, Uwe; Thiesen, Hans-Juergen; Colello, Raymond J.; Schwab, Martin E.
CS Brain Res. Inst., Univ. Zurich, Zurich, Switz.
SO J. Neurochem. (**1995**), 65(5), 1955-66
CODEN: JONRA9; ISSN: 0022-3042
DT Journal
LA English
AB The function of the vertebrate nervous system is dependent on the proper myelination of its fiber tracts. Myelin of the CNS is produced by oligodendrocytes. To identify gene regulatory **proteins** expressed in this particular glial cell type, cDNAs coding for **Cys2/His2 zinc finger** **proteins** were isolated from a rat oligodendrocyte cDNA library. One clone, named rKr2 (rKr for rat Krueppel-type **protein**), encodes a **protein** with 19 C-terminal **zinc** **finger** domains and an N-terminal Krueppel-assocd. box domain. This N-terminal domain of the rKr2 **protein** behaved as a strong transcriptional repressor module when fused to the **DNA-binding** domain of yeast GAL4 and tested on an appropriate reporter construct. High levels of rKr2 mRNA in adult rat tissues were found only in the CNS and testis; in the CNS, the message was predominantly expressed in differentiated oligodendrocytes. The modular structure of the rKr2 **protein** (C-terminal **DNA-binding** domain, N-terminal repressor module) and its expression pattern suggest that it acts as a sequence-specific transcriptional repressor in the myelin-producing glial cells of the CNS.
IT **172020-95-0 172020-96-1**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; **Cys2/His2 zinc** **finger** gene rKr2 is expressed in differentiated rat oligodendrocytes and encodes a protein with a functional repressor domain)

L57 ANSWER 22 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1995:856117 HCAPLUS
DN 123:248582
TI Derivatives of **zinc finger** nucleic acid-binding domains of transcription factors and their use in the modulation of gene expression
IN Barbas, Carlos F., III; Gottesfeld, Joel M.; Wright, Peter E.
PA Scripps Research Institute, USA
SO PCT Int. Appl., 135 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9519431	A1	19950720	WO 1995-US829	19950118 <--
	W: AU, CA, FI, JP, NO, US				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2181548	AA	19950720	CA 1995-2181548	19950118 <--
	AU 9516865	A1	19950801	AU 1995-16865	19950118 <--
	AU 704601	B2	19990429		
	EP 770129	A1	19970502	EP 1995-908614	19950118 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	JP 09508019	T2	19970819	JP 1995-519231	19950118 <--

	FI 9602879	A	19960917	FI 1996-2879	19960717 <--
	NO 9602991	A	19960918	NO 1996-2991	19960717 <--
	US 6242568	B1	20010605	US 1996-676318	19961230 <--
PRAI	US 1994-183119	A	19940118 <--		
	US 1994-312604	A	19940928 <--		
	WO 1995-US829	W	19950118 <--		

AB An assay for identification of novel transcription-modulating **zinc finger**-nucleotide binding polypeptides is described. These proteins are useful for inhibiting, activating or enhancing gene expression from a **zinc finger**-nucleotide binding motif contg. promoter or other transcriptional control element, as well as a structural gene or RNA sequence and so may be of therapeutic use. Novel **zinc finger**-nucleotide binding polypeptides are described. The assay measures the binding of a protein to **zinc finger**-binding site and so does not require detailed knowledge of the structure of the protein. A panel of randomly mutagenized genes for **zinc finger** proteins in a phage display library are panned against an array of **zinc finger recognition** sequences.

IT **169108-70-7 169108-73-0 169108-74-1**
169108-76-3
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(amino acid sequence; derivs. of **zinc finger** nucleic acid-binding domains of transcription factors and their use in modulation of gene expression)

IT **168971-84-4D**, analogs, derivs.
RL: MSC (Miscellaneous)
(**zinc finger** linker **peptide**; derivs. of **zinc finger nucleic acid-binding** domains of transcription factors and their use in modulation of gene expression)

L57 ANSWER 23 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1995:825211 HCAPLUS
DN 124:2339
TI Isolation and characterization of a novel **zinc-finger** protein with transcriptional repressor activity
AU Williams, Amy J.; Khachigian, Levon M.; Shows, Thomas; Collins, Tucker
CS Vascular Res. Div., Brigham and Women's Hosp. and Harvard Med. Sch., Boston, MA, 02115, USA
SO J. Biol. Chem. (**1995**), 270(38), 22143-52
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB To identify genes that can repress the expression of growth regulatory mols., a human fetal cDNA library was screened with a degenerate oligonucleotide that corresponds to the conserved stretch of 6 amino acids connecting successive **zinc-finger** regions in the Wilms' tumor suppressor/Egr-1 family of **DNA-binding proteins**. One clone, designated **zinc-finger protein** 174 (ZNF174), corresponds to a putative transcription factor with 3 **zinc fingers** and a novel **finger**-assocd. domain, designated the SCAN box. The three **Cys2-His2**-type **zinc fingers** are positioned at the C-terminus, whereas the 65-amino acid **finger**-assocd. SCAN box is located near the N-terminus. Chromosomal localization using somatic cell hybrid anal. and fluorescent in situ hybridization mapped the gene for ZNF174 to human chromosome 16p13.3. The 2.5-kb transcript from this gene is expressed in a variety of human organs, but most strongly in adult testis and ovary. Fusion of the upstream regulatory region of ZNF174 to the **DNA-binding** domain of GAL4 revealed that the gene could confer a repression function on the heterologous **DNA-binding** domain. ZNF174 selectively repressed reporter activity driven by the platelet-derived growth factor-B chain and transforming

growth factor-.beta.1 promoters and bound to **DNA** in a specific manner. This member of the C2H2-type **zinc-finger** family is a novel transcriptional repressor.

IT **171042-66-3**
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; isolation and characterization of **zinc-finger** protein ZNF174 with transcriptional repressor activity)

L57 ANSWER 24 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1995:230394 HCAPLUS
DN 122:49494
TI Cooperative, non-specific **binding** of a **zinc finger peptide** to **DNA**
AU Nedved, Michael L.; Moe, Gregory R.
CS Department Chemistry Biochemistry, University Delaware, Newark, DE, 19716, USA
SO Nucleic Acids Res. (**1994**), 22(22), 4705-11
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The **DNA binding** and structural properties of Xfin-31, a 25-amino acid **zinc finger peptide**, in the reduced, oxidized, and **zinc** complex forms, as well as the 14-residue helical segment of the **zinc finger** (residues 12-25) were compared using affinity coelectrophoresis (ACE) and CD spectroscopy. The **zinc** complex and oxidized **peptides** bind cooperatively to **DNA**, although the cooperativity factor, .omega., is >15-fold greater for the **zinc** complex. The reduced **peptide** in the absence of **zinc** and the helical segment do not bind cooperatively (.omega. = 1). Hence, the **binding** const. for singly contiguous sites (K.omega.) ranges over 100-fold for the various **peptides** even though the intrinsic **binding** consts. (K) are similar. An increase in **binding** order and affinity for the other forms of Xfin-31 is correlated with an increasing similarity of the CD spectrum to that of the Xfin-31 **zinc** complex. The surprising **DNA binding** activity of the oxidized **peptide** may result from hydrophobic interactions between the N-terminal loop formed by the Cys3-Cys6 disulfide bond and conserved hydrophobic residues in the C-terminal segment. Xfin-31 may be a particularly useful model for studying several poorly understood aspects of cooperative, nonspecific **DNA binding** since it is small, has a stable, well-defined structure, and structures of **zinc fingers** bound to **DNA** have been detd.

IT **123658-20-8 123714-99-8 123714-99-8D**, **zinc** complex
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(cooperative, nonspecific **binding** of a **zinc finger peptide** to **DNA**)

L57 ANSWER 25 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1995:195296 HCAPLUS
DN 122:48105
TI The zebrafish egr1 gene encodes a highly conserved, **zinc-finger** transcriptional regulator
AU Drummond, Iain A.; Rohwer-Nutter, Patricia; Sukhatme, Vikas P.
CS Department of Medicine, Harvard Medical School and Beth Israel Hospital, Boston, MA, 02215, USA
SO DNA Cell Biol. (**1994**), 13(10), 1047-55
CODEN: DCEBE8; ISSN: 1044-5498
DT Journal
LA English
AB The Egr family of transcriptional regulators comprise a group of genes which encode members of the **Cys2-His2** glass of **zinc-finger proteins**. The authors have isolated a zebrafish egr1 homolog by screening a zebrafish genomic library

with a mouse Egr1 **zinc finger** probe. Southern blotting indicated the existence of a single zebrafish erg1 gene and, as in higher vertebrates, the presence of related members of a larger gene family. Sequence anal. of the zebrafish erg1 coding region revealed a high level of homol. to the mouse, rat, and human Egr1 genes with the notable exception of a polymorphic, triplet nucleotide repeat sequence in the region coding for the amino terminus of the Egr1 **protein**. The predicted **DNA-binding, zinc-finger** domain **protein** sequence was strictly conserved. The 5' region of the zebrafish egr1 gene contained a variety of transcription factor **binding** sites, also present in the mouse gene, for serum response factor, CREB and c-Ets. The zebrafish egr1 transcript was approx. 3.4 kb in size and was expressed in adult zebrafish brain and muscle RNA, a pattern of expression similar to that obsd. in mice. The potential for zebrafish egr1 to function as a transcriptional regular was tested by constructing an expression vector contg. zebrafish egr1 coding sequences under the control of a cytomegalovirus promoter. This construct was found to activate transcription of a reporter plasmid bearing multiple Egr1 **binding** sites when transiently cotransfected into mouse 3T3 cells. These results indicate that the structure, regulation, and function of the Egr1 gene have been highly conserved during vertebrate evolution and suggest an important role for this gene in growth and development.

IT **159868-47-0**
RL: PRP (Properties)
(amino acid sequence; zebrafish egr1 gene encodes highly conserved **zinc-finger** transcriptional regulator involved in development)

L57 ANSWER 26 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1995:127012 HCAPLUS
DN 122:25024
TI The zebrafish egr1 gene encodes a highly conserved, **zinc-finger** transcriptional regulator
AU Drummond, Iain A.; Rohwer-Nutter, Patricia; Sukhatme, Vikas P.
CS Dep. Med., Harvard Med. Sch. and Beth Israel Hosp., Boston, MA, 02215, USA
SO DNA Cell Biol. (**1994**), 13(9), 953-61
CODEN: DCEBE8; ISSN: 1044-5498
DT Journal
LA English
AB The Egr family of transcriptional regulators comprises a group fo genes that encode members of the **Cys2-His2** class of **zinc finger proteins**. A zebrafish egr1 homolog was isolated by screening a zebrafish genomic library with a mouse egr1 **zinc finger** probe. Southern blotting indicated the existence of single zebrafish egr1 gene and, as in higher vertebrates, the presence of related members of a larger gene family. Sequence anal. of the zebrafish egr1 coding region revealed a high level of homol. to the mouse, rat, and human egr1 genes with the notable exception of a polymorphic, triplet and nucleotide repeat sequence in the region coding for the N-terminus of the egr1 **protein**. The predicted **DNA-binding, zinc finger** domain **protein** sequence was strictly conserved. The 5' region of the zebrafish egr1 gene contained a variety of transcription factor **binding** sites, also present in the mouse gene, for serum response factor, CREB, and c-ets. The zebrafish egr1 transcript was .apprx.3.4 kb size and was expressed in adult zebrafish brain and muscle RNA, a pattern of expression similar to that obsd. in mice. The potential for zebrafish egr1 to function as a transcriptional regulator was tested by constructing an expression vector contg. zebrafish egr1 coding sequences under the control of a cytomegalovirus promoter. This construct activated transcription of a receptor plasmid bearing multiple egr1 **binding** sites when transiently cotransfected into mouse 3T3 cells. The results indicate that the structure, regulation, and function of the egr1 gene have been highly conserved during vertebrate evolution and suggest an important role for this gene in growth and development.

IT **159868-47-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence and expression of the highly conserved zebrafish egr1 gene transcriptional regulator)

L57 ANSWER 27 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1994:673509 HCAPLUS
DN 121:273509
TI Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity
AU Garfinkel, Mark D.; Wang, Jhy; Liang, Yuanping; Mahowald, Anthony P.
CS Dep. Mol. Genet. Cell Biol., Univ. Chicago, Chicago, IL, 60637, USA
SO Mol. Cell. Biol. (**1994**), 14(10), 6809-18
CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB The Drosophila melanogaster shavenbaby (svb)-ovo gene region is a complex locus, contg. two distinct but comutable genetic functions. Ov is required for survival and differentiation of female germ line cells and plays a role in germ line sex detn. In contrast, svb is required in both male and female embryos for the prodn. of epidermal locomotor and sensory structures. Sequences required for the two genetic functions are partially overlapping. Ovo corresponds to a previously described germ line-dependent 5.0-kb poly(A)+ mRNA that first appears in the germarium and accumulates in nurse cells during oogenesis. The 5.0-kb mRNA is stored in the egg, but it is rapidly lost in the embryos except for its continued presence in the germ line precursor pole cells. The ovo mRNA predicts a 1028-amino-acid 110.6-kDa **protein** homologous with transcription factors. The authors have identified an embryonic mRNA, 7.1 kb in length, that contains exons partially overlapping those of the 5.0-kb poly(A)+ mRNA. The spatial distribution of this newly discovered transcript during midembryogenesis suggests that it corresponds to the svb function. The arrangement of exons common to the 5.0- and 7.1-kb mRNAs suggests that the Ovo and Svb **proteins** share **DNA-binding** specificity conferred by four **Cys2-His2 zinc finger** motifs but differ functionally in their capacity to interact with other components of the transcription machinery.
IT **158857-29-5**
RL: PRP (Properties)
(amino acid sequence; multiple products from shavenbaby-ovo gene region of Drosophila melanogaster and relationship to genetic complexity)

L57 ANSWER 28 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1994:185581 HCAPLUS
DN 120:185581
TI Independence of metal binding between tandem Cys2His2 **zinc finger** domains
AU Krizek, Beth Allyn; Zawadzke, Laura E.; Berg, Jeremy M.
CS Dep. Chem., Johns Hopkins Univ., Baltimore, MD, 21218, USA
SO Protein Sci. (**1993**), 2(8), 1313-9
CODEN: PRCIEI; ISSN: 0961-8368
DT Journal
LA English
AB Most Cys2His2 **zinc finger proteins** contain tandem arrays of metal **binding** domains. The tandem nature of these arrays suggests that metal **binding** by these domains may not be independent but rather that metal **binding** may occur in a cooperative manner. This is esp. true in light of the crystal structure of a three **zinc finger** array bound to **DNA** that revealed several types of interactions between domains. To address this question, **peptides** contg. two tandem domains have been prepd. While metal **binding** studies do show that the two **finger peptide** has a metal ion affinity about threefold higher than that for a single domain **peptide** with the same sequence, addnl. studies reveal that this behavior is due to increased

single site affinities in the context of the two domain **peptide** rather than to cooperativity. These studies indicate that domains of this type are independent of one another with regard to metal **binding**, at least in the absence of **DNA**. This observation has implications with regard to the question of whether the activities of **proteins** of this class might be modulated by available **zinc** concns.

IT **133551-05-0**
RL: BIOL (Biological study)
(cobalt binding to, in tandem **zinc finger** domain metal binding modeling)

IT **153613-05-9**, Peptide CP-CP(CCCC) (synthetic reduced) **153613-06-0**, Peptide CP-CP (synthetic reduced) **153613-07-1**, Peptide CP-X (synthetic reduced)
RL: BIOL (Biological study)
(cobalt binding to, in tandem **zinc finger** domain metal binding modeling, cooperativity in relation to)

L57 ANSWER 29 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1993:663879 HCAPLUS
DN 119:263879
TI The ht.beta. gene encodes a novel CACCC box-binding protein that regulates T-cell receptor gene expression
AU Wang, Yu Kang; Kobori, Joan A.; Hood, Leroy
CS Div. Biol., California Inst. Technol., Pasadena, CA, 91125, USA
SO Mol. Cell. Biol. (**1993**), 13(9), 5691-701
CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB A gene encoding a novel CACCC box-**binding protein** that binds to the promoter region of the human T-cell receptor (TCR) V.beta.8.1 gene and the mouse TCR .alpha. gene silencer has been cloned. This gene, termed ht.beta., contains 4 **zinc fingers** of the class **Cys2**-X12-**His2** that may be responsible for **DNA binding** and a highly neg. charged region that defines a putative transcriptional activation domain. Anal. of the expression of ht.beta. mRNA revealed similar expression levels and patterns in various cells lines. The bacterially expressed ht.beta. **protein** can bind to the CACCC box in both the human TCR V.beta.8.1 gene promoter and the mouse TCR .alpha. gene silencer. The CACCC box is essential for efficient transcription of the V.beta.8.1 promoter. Cotransfection with an ht.beta. expression plasmid and a reporter vector indicated that ht.beta. can activate human transcription. Ht.beta. also is able to counteract the silencing effect of the mouse TCR .alpha. gene silencer. The CACCC box has been found in almost all V.beta.8.1 gene subfamily members and in both TCR .alpha. and .beta. gene enhancers in humans and mice. These results suggest that the CACCC box-**binding protein** may have an important regulatory function of TCR gene expression in .alpha..beta. T cells vs. .gamma..delta. T cells.

IT **151442-11-4**
RL: PRP (Properties)
(amino acid sequence of and T-cell receptor gene expression regulation by)

L57 ANSWER 30 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1993:511528 HCAPLUS
DN 119:111528
TI Adjacent **zinc-finger** motifs in multiple **zinc -finger** peptides from SWI5 form structurally independent, flexibly linked domains
AU Nakaseko, Yukinobu; Neuhaus, David; **Klug, Aaron**; Rhodes, Daniela
CS Lab. Mol. Biol., MRC, Cambridge, CB2 2QH, UK
SO J. Mol. Biol. (**1992**), 228(2), 619-36
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English

AB **Peptides** contg. either one, two or three of the three **zinc-finger** motifs from the yeast transcription factor SWI5 have been prepd. by expression in Escherichia coli. The **DNA binding** characteristics of these **peptides** were investigated, and a two-dimensional NMR study undertaken to establish the three-dimensional structures of the two-**finger peptide** . The **peptide** contg. **fingers** 1 and 2 binds sequence specifically to two thirds of the **DNA binding** site **recognized** either by intact SWI5 or by the isolated three-**finger peptide**, and hence has the correct tertiary fold for **DNA recognition**. These results also establish the polarity of **DNA binding**, since the N-terminal two **fingers** of SWI5 bind to the 5' end of the **DNA binding** site. Mild proteolysis of the three-**finger peptide** using trypsin results in a small no. of discrete products, which is consistent with the presence of three structured mini-domains. Nearly complete NMR signal assignments were obtained for two **peptides** contg. **finger** 2 alone or **fingers** 1 + 2. Comparison of two-dimensional spectra of these **peptides** and others clearly shows that the NOE enhancements and chem. neighboring **fingers**. This clearly indicates that adjacent **zinc-finger** domains are structurally independent in these **peptides** from SWI5. However, there must be some steric limitations on the possible relative orientations of the **fingers** , and to establish limits for these a set of structures for the **peptide** contg. **fingers** 1 + 2 was calcd. using the YASAP simulated annealing protocol in conjunction with NMR-based constraints. A more detailed description of the three-dimensional structures of **finger** 1 and **finger** 2, and their relationship to other previously detd. structures of single **zinc-fingers**, is given in the accompanying paper.

IT **128086-74-8 128087-09-2 146836-66-0**
146836-68-2
RL: BIOL (Biological study)
(soln. structure and stability and DNA-binding properties of, as yeast SWI5 transcription factor **zinc-finger** motif model)

IT **149348-55-0 149348-56-1**
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(soln. structure and stability and DNA-binding properties of, as yeast SWI5 transcription factor **zinc-finger** motif model)

L57 ANSWER 31 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1993:444590 HCAPLUS
DN 119:44590
TI Use of a **zinc-finger consensus** sequence framework and specificity rules to design specific **DNA binding proteins**
AU Desjarlais, John R.; Berg, Jeremy M.
CS Thomas C. Jenkins Dep. Biophys., Johns Hopkins Univ., Baltimore, MD, 21218, USA
SO Proc. Natl. Acad. Sci. U. S. A. (**1993**), 90(6), 2256-60
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Three **zinc-finger proteins** with different **DNA-binding** specificities were designed. The design strategy combines a consensus **zinc-finger** framework sequence with previously characterized **recognition** regions such that the specificity of each **protein** is predictable. The 1st **protein** consists of 3 identical **zinc fingers**, each of which was expected to **recognize** the subsite GCG. This **protein** binds specifically to the sequence 5'-GCG-GCG-GCG-3' with a dissocn. const. of .apprxeq.11 .mu.M. The 2nd **protein** has 3 **zinc fingers** with different predicted preferred subsites. This **protein** binds to the predicted

recognition site 5'-GGG-GCG-GCT-3' with a dissocn. const. of 2 nM. Furthermore, selection expts. indicate that this is the optimal **binding** site. A permuted version of the 2nd **protein** was also constructed and shown to preferentially **recognize** the corresponding permuted site 5'-GGG-GCT-GCG-3' over the nonpermuted site. These results indicate that earlier observations on the specificity of **zinc fingers** can be extended to generalized **zinc -finger** structures and realize the use of **zinc fingers** for the design of site-specific **DNA-binding proteins**. This consensus-based design system provides a useful model system with which to study details of **zinc -finger-DNA** specificity.

IT **148023-61-4, Protein** QDR-RER-RHR (synthetic **DNA -binding** reduced) **148023-62-5, Protein** RER-QDR-RHR (synthetic **DNA-binding** reduced)
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(design and **DNA binding** by **zinc-finger** motif in relation to)

IT **148023-60-3, Protein** RER-RER-RER (synthetic **DNA -binding** reduced)
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(design and **DNA binding** by, **zinc-finger** motif in relation to)

L57 ANSWER 32 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1993:403327 HCAPLUS
DN 119:3327
TI A novel human insulinoma-associated cDNA, IA-1, encodes a **protein** with **"zinc-finger" DNA-binding** motifs
AU Goto, Yasuhiro; De Silva, Mark G.; Toscani, Antonio; Prabhakar, Bellur S.; Notkins, Abner Louis; Lan, Michael S.
CS Lab. Oral Med., Natl. Inst. Dent. Res., Bethesda, MD, 20892, USA
SO J. Biol. Chem. (**1992**), 267(21), 15252-7
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB A subtraction library was constructed from human insulinoma (.beta. cell tumor) and glucagonoma (.alpha. cell tumor) cDNA phagemid libraries. Differential screening of 153 clones with end-labeled mRNAs from insulinoma, glucagonoma, and HeLa cells resulted in the isolation of a novel cDNA clone designated IA-1. This cDNA clone has a 2838-base pair sequence consisting of an open reading frame of 1530 nucleotides, which translated into a **protein** of 510 amino acids with a pI value of 9.1 and a mol. mass of 52,923 daltons. At the 3'-untranslated region there are seven ATTTA sequences between 2 polyadenylation signals (AATAAA). The IA-1 **protein** can be divided into 2 domains based upon the features of its amino acid sequence. The N-terminal domain of the deduced **protein** sequence (amino acids 1-250) has 4 classical pro-hormone dibasic conversion sites and an amidation signal sequence, Pro-Gly-Lys-Arg. The C-terminal domain (amino acids 251-510) contains five putative **zinc-finger DNA-binding** motifs of the form X3-Cys-X2-4-Cys-X12-His-X3-4-His-X4 which has been described as a consensus sequence for members of the **Cys2-His2 DNA-binding protein** class. Northern blot anal. revealed IA-1 mRNA in 5 of 5 human insulinoma and 3 of 3 murine insulinoma cell lines. Expression of this gene was undetectable in normal tissues. Addnl. tissue studies revealed that the message is expressed in several tumor cell lines of neuroendocrine origin including pheochromocytoma, medullary thyroid carcinoma, insulinoma, pituitary tumor, and small cell lung carcinoma. The restricted tissue distribution and unique sequence motifs suggest that this novel cDNA clone may encode a **protein** assocd. with the transformation of neuroendocrine cells.

IT **147955-03-1**, Protein (human clone IA-1 insulinoma-associated reduced)
RL: PRP (Properties)
(amino acid sequence of, complete)

L57 ANSWER 33 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1993:185997 HCAPLUS
DN 118:185997
TI Characterization of a **zinc finger DNA-binding protein** expressed specifically in Petunia petals and seedlings
AU Takatsuji, Hiroshi; Mori, Masaki; Benfey, Philip N.; Ren, Ling; Chua, Nam Hai
CS Lab. Plant Mol. Biol., Rockefeller Univ., New York, NY, 10021, USA
SO EMBO J. (**1992**), 11(1), 241-9
CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB In Petunia, the expression of the 5-enolpyruvylshikimate-3-phosphate synthase gene (EPSPS) is tissue-specific and developmentally regulated. Nuclear exts. from Petunia petal contain a factor that interacts with the 5'-upstream region of EPSPS. DNase I footprinting expts. revealed 4 strong **binding** sites (EP1-EP4) and several weaker sites that appear to bind the same factor. A cDNA (EPF1) encoding a **DNA-binding protein** that has similar **binding** activity to that of the nuclear factor was isolated. The deduced amino acid sequences shows that the encoded **protein**, EPF1, contains 2 repeats of a **Cys2/His2 zinc finger** motif. EPF1 and the factor detected in nuclear exts. differ in their mol. wt. and Zn2+ requirements. Nevertheless, Northern blot analyses showed that the expression pattern of EPF1 is remarkably similar to that of EPSPS. In addn., as detd. by translational fusion of the EPF1 upstream region to the .beta.-glucuronidase reporter gene, the cell- specific expression pattern of EPF1 in flower and seedling nearly identical to that of EPSPS. Taken together with the results of cis-element analyses, these observations suggest that EPF1 may be one of the factors involved in the activation of EPSPS.
IT **146989-67-5**
RL: PRP (Properties)
(amino acid sequence of, complete)

L57 ANSWER 34 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1993:18158 HCAPLUS
DN 118:18158
TI Clone pAT 133 identifies a gene that encodes another human member of a class of growth factor-induced genes with almost identical **zinc-finger** domains
AU Mueller, Hans Joachim; Skerka, Christine; Bialonski, Alexandra; Zipfel, Peter F.
CS Bernhard Nocht Inst. Trop. Med., Hamburg, 2000/36, Germany
SO Proc. Natl. Acad. Sci. U. S. A. (**1991**), 88(22), 10079-83
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The structure and regulation of a gene represented by clone pAT 133, which is induced upon transition from a resting state (G0) through the early phase of the cell cycle (G1), is reported. The pAT 133 gene is immediately induced, with FOS-like kinetics, in human T cells and in fibroblasts. Primary structure anal. showed that the encoded protein contains 3 tandem **Zn-finger** sequences of the type **Cys2**-Xaa12-**His2**. This **Zn-finger** region, which is thought to bind DNA in a sequence-specific manner, was similar (>80% on the amino acid level) to 2 previously described transcription factors, pAT 225/EGR1 and pAT 591/EGR2. Except for the conserved **Zn-finger** domains, the amino acid sequences of the 3 proteins were distinct. This structural similarity suggested

that the pAT 133 gene encodes a transcription factor with a specific biol. function. Comparing the regulation of these related **Zn-finger**-encoding genes showed coordinate induction upon mitogenic stimulation of resting T lymphocytes and of resting fibroblasts. However, upon transition from a proliferating (G1) to a resting state of the cell cycle the 3 genes were differently regulated. In human histiocytic U937 cells, mRNA of clone pAT 133 was constitutively expressed, whereas mRNA of pAT 225/EGR1 was induced upon induction of terminal differentiation. In contrast, mRNA representing pAT 591/EGR2 was not expressed in these cells. This difference in gene regulation suggests distinct biol. roles in the control of cell proliferation for the resp. proteins.

IT **144997-43-3**, Protein (human clone pAT133-17/pAT133-15 50.6-kilodalton reduced)
RL: PRP (Properties)
(amino acid sequence of, complete)

L57 ANSWER 35 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1992:145140 HCAPLUS
DN 116:145140
TI The early response gene NGFI-C encodes a **zinc finger** transcriptional activator and is a member of the GCGGGGGCG (GSG) element-binding protein family
AU Crosby, Seth D.; Puetz, John J.; Simburger, Kelli S.; Fahrner, Timothy J.; Milbrandt, Jeffrey
CS Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SO Mol. Cell. Biol. (**1991**), 11(8), 3835-41
CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB A nerve growth factor-induced early-response gene encodes a **Cys2 /His2 zinc finger protein** NGFI-C.
RNA blot anal. demonstrates that NGFI-C mRNA is induced within minutes of stimulation of PC12 cells by nerve growth factor and is similarly activated in brain after a Metrazol-induced seizure. The cDNA sequence predicts a **protein** that contains three **zinc fingers** which show striking homol. to the **DNA-binding** regions of three previously reported **zinc finger proteins**, NGFI-A, Krox-20, and the Wilms' tumor gene product. NGFI-C binds to the previously described **DNA-binding** site of these three **proteins**, which is GCGGGGGCG. Cotransfection expts. revealed that NGFI-C strongly activates transcription from this site in mammalian cells. The isolation of another early-response gene that encodes a member of the G(C/G)G or GSG element-**binding** family should provide an opportunity to investigate the relative contributions of a family of transcription factors to the cell's response to changes in its environment.

IT **139874-91-2**, Ribonucleic acid formation factor NGFI-C (rat clone pCMV-NGFI-C reduced)
RL: PRP (Properties)
(amino acid sequence of)

L57 ANSWER 36 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1990:492265 HCAPLUS
DN 113:92265
TI A **DNA-binding protein** containing two widely separated **zinc finger motifs** that **recognize** the same **DNA** sequence
AU Fan, Chen Ming; Maniatis, Tom
CS Dep. Biochem. Mol. Biol., Harvard Univ., Cambridge, MA, 02138, USA
SO Genes Dev. (**1990**), 4(1), 29-42
CODEN: GEDEEP; ISSN: 0890-9369
DT Journal
LA English
AB A full-length cDNA clone was isolated which encodes a **protein** (PRDII-BF1) that binds specifically to a pos. regulatory domain (PRDII) of the human IFN-.beta. gene promoter, and to a similar sequence present in a

no. of other promoters and enhancers. The sequence of this **protein** reveals two novel structural features. First, it is the largest sequence-specific **DNA-binding protein** reported to data (298 kD). Second, it contains two widely sepd. sets of C2-H2-type **zinc fingers**. Remarkably, each set of **zinc fingers** binds to the same **DNA** sequence motif with similar affinities and methylation interference patterns. Thus, this **protein** may act by **binding** simultaneously to reiterated copies of the same **recognition** sequence. Although the function of PRDII-BF1 is not known, the level of its mRNA is inducible by serum and virus, albeit with different kinetics.

IT **128826-24-4**
RL: PRP (Properties)
(amino acid sequence of)

L57 ANSWER 37 OF 37 HCAPLUS COPYRIGHT 2002 ACS
AN 1989:226313 HCAPLUS
DN 110:226313
TI Molecular cloning, sequencing, and mapping of EGR2, a human early growth response gene encoding a protein with "**zinc**-binding **finger**" structure
AU Joseph, Loren J.; Le Beau, Michelle M.; Jamieson, Gordon A., Jr.; Acharya, Sonia; Shows, Thomas B.; Rowley, Janet D.; Sukhatme, Vikas P.
CS Howard Hughes Med. Inst., Univ. Chicago, Chicago, IL, 60637, USA
SO Proc. Natl. Acad. Sci. U. S. A. (**1988**), 85(19), 7164-8
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Early growth response gene-1 (Egr-1) is a mouse gene displaying fos-like induction kinetics in diverse cell types following mitogenic stimulation. Egr-1 encodes a **protein** with **zinc-binding finger** structure. **Zinc fingers** are a **protein** structural motif that serve as **DNA-binding** domains in several transcriptional regulatory **proteins**. Using low-stringency hybridization with an Egr-1 cDNA probe, a distinct human cDNA (designated EGR2 for early growth response gene-2) was identified, which is coregulated with EGR1 by fibroblast and lymphocyte mitogens; however, several stimuli that induce Egr-1 mRNA in PC12 (rat pheochromocytoma) cells do not induce Egr-2 mRNA. The cDNA sequence predicts a **protein** of 406 amino acids, including 3 tandem **zinc fingers** of the **Cys2-His2** class. Strikingly, the deduced amino acid sequences of human EGR2 and mouse Egr-1 are 92% identical in the **zinc finger** region but show no similarity elsewhere. EGR2 Maps to human chromosome 10 at bands q21-22. Structure-function anal. of EGR2 and EGR1 **proteins** should provide insight into the mechanisms linking signal transduction and transcriptional regulation of gene expression.
IT **120718-61-8**, Protein (human clone ZAP2/ZAP8/ZAP32 gene EGR2 reduced) **120718-62-9**, Protein (mouse clone Krox-20 gene EGR2 reduced)
RL: PRP (Properties)
(amino acid sequence of)

=> d all 38-49

L74 ANSWER 38 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1998:448099 BIOSIS
DN PREV199800448099
TI Comprehensive DNA recognition through concerted interactions from adjacent **zinc fingers**.
AU **Isalan, Mark; Klug, Aaron; Choo, Yen (1)**
CS (1) MRC Lab. Molecular Biol., Hills Road, Cambridge CB2 2QH UK
SO Biochemistry, (**Sept. 1, 1998**) Vol. 37, No. 35, pp. 12026-12033.
ISSN: 0006-2960.
DT Article

LA English
AB **Zinc fingers** are small **DNA-binding** modules noted for their occurrence in a large number of eukaryotic transcription factors, and their use in **protein** engineering. Although it was expected that **zinc fingers** can bind to a wide diversity of **DNA** sequences, previous studies using model **zinc finger** domains from Zif268 (and Sp1) have revealed a potential limitation to the **DNA-binding** specificity. For example, phage display selection of individual **zinc fingers** to recognize trinucleotide **DNA** subsites returned **fingers** that bound specifically only to triplets of the form GNN, i.e., triplets with guanine at the 5' end. Following our recently reported work (Isalan, M., Choo, Y., and Klug, A. (1997) Proc. Natl. Acad Sci. U.S.A. 94, 5617 -5621), we now show that this limitation can be overcome by the concerted randomization of certain amino acid positions in adjacent **zinc fingers** that specify overlapping **DNA** subsites. This illustrates an important mechanism underlying **DNA** recognition by arrays of **zinc fingers**, and points the way to improved strategies for the design of highly specific **zinc finger proteins** that bind any given nucleotide sequence.
CC Genetics and Cytogenetics - General *03502
Biochemical Studies - General *10060
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
zinc finger: DNA-binding specificity; DNA: comprehensive recognition
IT Miscellaneous Descriptors
DNA-**zinc finger** interaction

L74 ANSWER 39 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1997:295637 BIOSIS
DN PREV199799594840
TI Synergy between adjacent **zinc fingers** in sequence-specific DNA recognition.
AU **Isalan, Mark; Choo, Yen (1); Klug, Aaron**
CS (1) Med. Res. Council Lab. Molecular Biol., Hills Rd., Cambridge CB2 2QH UK
SO Proceedings of the National Academy of Sciences of the United States of America, (1997) Vol. 94, No. 11, pp. 5617-5621. ISSN: 0027-8424.
DT Article
LA English
AB Zif268-like **zinc fingers** are generally regarded as independent **DNA-binding** modules that each specify three base pairs in adjacent, but discrete, subsites. However, crystallographic evidence suggests that a contact also can occur from the second helical position of one **finger** to the subsite of the preceding **finger**. Here we show for the three-**finger** **DNA-binding** domain of the **protein** Zif268, and a panel of variants, that deleting the putative contact from **finger** 3 can affect the **binding** specificity for the 5' base in the adjoining triplet, which forms part of the **binding** site of **finger** 2. This finding demonstrates that Zif268-like **zinc fingers** can specify overlapping 4-bp subsites, and that sequence specificity at the boundary between subsites arises from synergy between adjacent **fingers**. This has important implications for the design and selection of **zinc fingers** with novel **DNA binding** specificities.
CC Genetics and Cytogenetics - General *03502
Comparative Biochemistry, General *10010
Biochemical Methods - General *10050
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - Minerals *10069
Replication, Transcription, Translation *10300

Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
Metabolism - General Metabolism; Metabolic Pathways *13002
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
BC Enterobacteriaceae *06702
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Metabolism; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics); Physiology
IT Miscellaneous Descriptors
ANALYTICAL METHOD; CRYSTALLOGRAPHY; DNA; DNA-BINDING MODULES; DNA-BINDING SPECIFICITIES; MOLECULAR GENETICS; SEQUENCE-SPECIFIC DNA RECOGNITION; STRAIN-TG1; TRANSCRIPTION FACTORS; **ZINC FINGERS**
ORGN Super Taxa
Enterobacteriaceae: Eubacteria, Bacteria
ORGN Organism Name
Escherichia coli (Enterobacteriaceae)
ORGN Organism Superterms
bacteria; eubacteria; microorganisms

L74 ANSWER 40 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1998:32703 BIOSIS
DN PREV199800032703
TI Promoter-specific activation of gene expression directed by bacteriophage-selected **zinc fingers**.
AU **Choo, Y. (1)**; Castellanos, A.; Garcia-Hernandez, B.; Sanchez-Garcia, I.; **Klug, A.**
CS (1) Med. Res. Counc. Lab. Mol. Biol., Hills Road, Cambridge CB2 2QH UK
SO Journal of Molecular Biology, (**Oct. 31, 1997**) Vol. 273, No. 3, pp. 525-532.
ISSN: 0022-2836.
DT Article
LA English
AB It has been shown that sequence-specific **DNA-binding** domains containing **zinc fingers** can be selected from libraries displayed on filamentous bacteriophage. The affinity and specificity of these **peptides** are well characterised in vitro, but few data are available to demonstrate specific **DNA binding** and discrimination between closely related **DNA** sequences in vivo. Transient transactivation assays were performed in mammalian cells, using expression plasmids which produce different amounts of a model transcription factor containing a phage-selected **zinc finger DNA-binding** domain, and reporter plasmids which carry systematic variations of the promoter sequence. When the intracellular concentration of the transcription factor was appropriate, activation of gene expression was absolutely dependent on a promoter having the same **DNA** sequence as that originally used to select the **zinc finger** domain by phage display. However, excessive intracellular concentrations of the transcription factor resulted in some less-specific **DNA binding**, leading to gene activation from similar promoters containing a maximum of two base changes. Thus, provided delivery is carefully controlled, highly specific control of gene expression in vivo can be achieved using artificial transcription factors containing phage-selected **zinc finger DNA-binding** domains.
CC Genetics and Cytogenetics - General *03502
Biochemical Studies - General *10060
Genetics of Bacteria and Viruses *31500
BC Bacterial Viruses - General 02700
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
artificial transcription factors; DNA binding domain
IT Miscellaneous Descriptors

bacteriophage-selected **zinc fingers**; gene expression: promoter-specific activation; DNA binding
ORGN Super Taxa
Bacterial Viruses: Viruses, Microorganisms
ORGN Organism Name
filamentous bacteriophage (Bacterial Viruses)
ORGN Organism Superterms
Bacterial Viruses; Microorganisms; Viruses

L74 ANSWER 41 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:519061 BIOSIS
DN PREV199598533361
TI Gene regulatory proteins and their interaction with DNA.
AU **Klug, Aaron**
CS MRC Lab. Molecular Biology, Cambridge CB2 2QH UK
SO Chambers, D. A. [Editor]. Annals of the New York Academy of Sciences, (1995) Vol. 758, pp. 143-160. Annals of the New York Academy of Sciences; DNA: The double helix: Perspective and prospective at forty years. Publisher: New York Academy of Sciences 2 East 63rd Street, New York, New York 10021, USA.
Meeting Info.: Conference Chicago, Illinois, USA October 13-16, 1993
ISSN: 0077-8923. ISBN: 0-89766-906-1 (paper), 0-89766-905-3 (cloth).
DT Book; Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Replication, Transcription, Translation *10300
Biophysics - Molecular Properties and Macromolecules *10506
Biophysics - Membrane Phenomena *10508
Endocrine System - General *17002
IT Major Concepts
Biochemistry and Molecular Biophysics; Endocrine System (Chemical Coordination and Homeostasis); Genetics; Membranes (Cell Biology); Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
LEUCINE
IT Miscellaneous Descriptors
BASIC LEUCINE ZIPPER; BETA-RIBBON MOTIF; BOOK CHAPTER; GENE EXPRESSION CONTROL; HELIX-TURN-HELIX MOTIF; HOMEODOMAIN **PROTEIN**; HORMONE RECEPTOR **DNA-BINDING** DOMAIN; MEETING PAPER; MOLECULAR MODEL; MOLECULAR RECOGNITION; TATA-BOX **BINDING PROTEIN**; THREE-DIMENSIONAL STRUCTURE; TRANSCRIPTION FACTOR; **ZINC FINGER PROTEIN**
RN 61-90-5 (LEUCINE)

L74 ANSWER 42 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:340395 BIOSIS
DN PREV199598354695
TI **Zinc fingers.**
AU **Klug, Aaron (1)**; Schwabe, John W. R.
CS (1) MRC Lab. Molecular Biology, Hills Road, Cambridge CB2 2QH UK
SO FASEB Journal, (1995) Vol. 9, No. 8, pp. 597-604.
ISSN: 0892-6638.
DT General Review
LA English
AB The term **zinc finger** was first used to describe a 30-residue, repeated sequence motif found in an unusually abundant Xenopus transcription factor. It was proposed that each motif is folded around a central **zinc** ion to form an independent minidomain and that adjacent **zinc fingers** are combined as modules to make up a **DNA-binding** domain with the modules "gripping" the **DNA** (hence the term **finger**). We now know that these proposals were correct and that these **DNA-binding**

motifs are found in many eukaryotic **DNA-binding proteins**. More recently, crystal structures of three different complexes between **zinc finger** domains and their target **DNA binding** sites have revealed a remarkably simple mode of interaction with **DNA**. The simplicity of the **zinc finger** structure, and of its interaction with **DNA**, is a very striking feature of this **protein** domain. After the discovery of the **zinc finger** motif, patterns of potential **zinc** ligands have been found in several other **proteins**, some of which also bind to **DNA**. Structural studies of these domains have revealed how **zinc** can stabilize quite diverse **protein** architectures. In total, 10 such small **zinc-binding** domains have been studied structurally. These form a diverse collection, but each in turn has been termed a **zinc finger** motif -although clearly what they have in common is only their **zinc-binding** property, which stabilizes an apparently autonomously folded unit.

CC Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - Minerals *10069
Replication, Transcription, Translation *10300
Biophysics - Molecular Properties and Macromolecules *10506
Biophysics - Membrane Phenomena *10508
Endocrine System - General *17002
Virology - Animal Host Viruses *33506
BC Retroviridae *02623
IT Major Concepts
Biochemistry and Molecular Biophysics; Endocrine System (Chemical Coordination and Homeostasis); Genetics; Membranes (Cell Biology); Microbiology; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Miscellaneous Descriptors
DNA-BINDING MOTIF; LIM DOMAIN; NUCLEAR HORMONE RECEPTOR; NUCLEOCAPSID **PROTEIN**; **PROTEIN** FOLDING; SECONDARY STRUCTURE; TRANSCRIPTION FACTOR; ZINC **BINDING** DOMAIN
ORGN Super Taxa
Retroviridae: Viruses
ORGN Organism Name
human immunodeficiency virus (Retroviridae)
ORGN Organism Superterms
microorganisms; viruses

L74 ANSWER 43 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:419418 BIOSIS
DN PREV199598433718
TI **Designing DNA-binding proteins** in the surface of filamentous phage.
AU **Choo, Yen; Klug, Aaron**
CS Med. Res. Counc., Lab. Mol. Biol., Hills Road, Cambridge CB2 2QH UK
SO Current Opinion in Biotechnology, (1995) Vol. 6, No. 4, pp. 431-436. ISSN: 0958-1669.
DT Article
LA English
CC Comparative Biochemistry, General *10010
Biochemical Methods - General *10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Replication, Transcription, Translation *10300
Biophysics - Molecular Properties and Macromolecules *10506
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Proteins, Peptides and Amino Acids *13012

Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
Genetics of Bacteria and Viruses *31500
Microbiological Apparatus, Methods and Media *32000
Virology - Bacteriophage *33504
BC Bacterial Viruses - General *02700
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Metabolism; Methods and Techniques; Microbiology; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Miscellaneous Descriptors
BIOTECHNOLOGY; DNA PROTEIN INTERACTIONS; MOLECULAR EVOLUTION; MOLECULAR STRUCTURE; PHAGE DISPLAY; PROTEIN ENGINEERING
ORGN Super Taxa
Bacterial Viruses - General: Viruses
ORGN Organism Name
bacterial viruses (Bacterial Viruses - General)
ORGN Organism Superterms
microorganisms; viruses

L74 ANSWER 44 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:34477 BIOSIS
DN PREV199598048777
TI Toward a code for the interactions of **zinc fingers** with DNA: Selection of randomized **fingers** displayed on phage.
AU **Choo, Yen; Klug, Aaron**
CS Med. Res. Council, Lab. Mol. Biol., Hills Rd., Cambridge CB2 2QH UK
SO Proceedings of the National Academy of Sciences of the United States of America, (1994) Vol. 91, No. 23, pp. 11163-11167.
ISSN: 0027-8424.
DT Article
LA English
AB We have used two selection techniques to study sequence-specific **DNA** recognition by the **zinc finger**, a small, modular **DNA-binding** minidomain. We have chosen **zinc fingers** because they bind as independent modules and so can be linked together in a **peptide** designed to bind a predetermined **DNA** site. In this paper, we describe how a library of **zinc** ringers displayed on the surface of bacteriophage enables selection of **fingers** capable of **binding** to given **DNA** triplets. The amino acid sequences of selected ringers which bind the same triplet are compared to examine how sequence-specific **DNA** recognition occurs. Our results can be rationalized in terms of coded interactions between **zinc** ringers and **DNA**, involving base contacts from a few a-helical positions. In the paper following this one, we describe a complementary technique which confirms the identity of amino acids capable of **DNA** sequence discrimination from these positions.
CC Genetics and Cytogenetics - General *03502
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - Molecular Properties and Macromolecules *10506
Genetics of Bacteria and Viruses *31500
Virology - Bacteriophage *33504
BC Bacterial Viruses - General *02700
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Methods and Techniques
IT Miscellaneous Descriptors
GENETIC ENGINEERING; METHOD; SEQUENCE SPECIFIC RECOGNITION
ORGN Super Taxa
Bacterial Viruses - General: Viruses
ORGN Organism Name
bacterial viruses (Bacterial Viruses - General)
ORGN Organism Superterms
microorganisms; viruses

L74 ANSWER 45 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:59043 BIOSIS
DN PREV199598073343
TI In vivo repression by a site-specific **DNA-binding** **protein** designed against an oncogenic sequence.
AU **Choo, Yen**; Sanchez-Garcia, Isidro; **Klug, Aaron**
CS Med. Res. Council, Lab. Mol. Biol., Hills Rd., Cambridge CB2 2QH UK
SO Nature (London), (1994) Vol. 372, No. 6507, pp. 642-645.
ISSN: 0028-0836.
DT Article
LA English
AB A **DNA-binding peptide** comprising three **zinc-fingers** has been engineered to bind specifically to a unique nine-base-pair region of a BCR-ABL fusion oncogene In preference to the parent genomic sequences. **Binding** to the target oncogene in chromosomal **DNA** is possible In transformed cells in culture, and results in blockage of transcription. Consequently, murine cells rendered independent of growth factors by the action of the oncogene revert to factor dependence upon transient transfection with a vector expressing the **peptide**.
CC Cytology and Cytochemistry - Animal 02506
Genetics and Cytogenetics - Animal *03506
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - Molecular Properties and Macromolecules *10506
Neoplasms and Neoplastic Agents - Biochemistry *24006
BC Muridae *86375
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Methods and Techniques; Tumor Biology
IT Miscellaneous Descriptors
BCR-ABL FUSION ONCOGENE; CANCER RESEARCH IMPLICATIONS; CHROMOSOMAL **DNA**; IN-VIVO **BINDING**; **PROTEIN** ENGINEERING
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae)
ORGN Organism Superterms
animals; chordates; mammals; nonhuman mammals; nonhuman vertebrates; rodents; vertebrates

L74 ANSWER 46 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1993:432622 BIOSIS
DN PREV199396087247
TI A role in DNA binding for the linker sequences of the first three **zinc fingers** of TFIIIA.
AU **Choo, Yen; Klug, Aaron**
CS Med. Res. Council, Lab. Mol. Biol., Cambridge CB2 2QH UK
SO Nucleic Acids Research, (1993) Vol. 21, No. 15, pp. 3341-3346.
ISSN: 0305-1048.
DT Article
LA English
AB **Zinc fingers** of the TFIIIA type are connected by short linker sequences between the structural units. Structural investigations by 2D NMR in solution and by X-ray crystallographic analyses of complexes with **DNA** point to a passive role for the linkers. We have therefore investigated the influence of the linker sequence on **DNA** **binding** using as a model the first three **fingers** of the **protein** TFIIIA. Insertion of certain heterologous linkers abolishes **binding**, and replacement of individual amino acids can reduce **binding** by factors of up to twenty-four.
CC Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - Minerals 10069

Biophysics - Molecular Properties and Macromolecules *10506
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics
IT Miscellaneous Descriptors
CONDENSED STRUCTURE FORMATION; DNA COLLAPSE; DNA TRANSFER METHOD; GENE TRANSFER; MOLECULE DELIVERY; POSITIVELY CHARGED LIPID BILAYER

L74 ANSWER 47 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1994:126855 BIOSIS
DN PREV199497139855
TI Co-chairman's remarks: Protein designs for the specific recognition of DNA.
AU **Klug, Aaron**
CS MRC Lab. Molecular Biol., Hills Road, Cambridge CB2 2QH UK
SO Gene (Amsterdam), (1993) Vol. 135, No. 1-2, pp. 83-92.
ISSN: 0378-1119.
DT Article
LA English
AB The selective expression of a gene is achieved through the interaction of **protein** transcription factors with characteristic nucleotide sequences located in the regulatory region of the gene, which is usually distinct from the coding region. These **proteins** contain domains which bind specifically to the **DNA** sites (or response elements). Some general principles in the design of these **DNA-binding** domains are described, followed by examples of the different structural classes discovered so far and how they recognise their **binding** sites.
CC Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biophysics - Molecular Properties and Macromolecules *10506
Biophysics - Membrane Phenomena *10508
BC *00500
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Membranes (Cell Biology)
IT Chemicals & Biochemicals
LEUCINE
IT Miscellaneous Descriptors
HELIX-TURN-HELIX; HOMEODOMAIN; HORMONE RECEPTORS; LEUCINE ZIPPER; MODULAR DESIGN; **ZINC FINGERS**
ORGN Organism Name
organisms (Organisms - Unspecified)
RN 61-90-5 (LEUCINE)

L74 ANSWER 48 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1993:95056 BIOSIS
DN PREV199395050252
TI Solution structures of two **zinc-finger** domains from SWI5 obtained using two-dimensional proton nuclear magnetic resonance spectroscopy: A **zinc-finger** structure with a third strand of beta-sheet.
AU Neuhaus, David (1); Nakaseko, Yukinobu; Schwabe, John W. R. (1); **Klug, Aaron (1)**
CS (1) MRC Lab. Molecular Biol., Hills Rd., Cambrdige CB2 2QH England
SO Journal of Molecular Biology, (1992) Vol. 228, No. 2, pp. 637-651.
ISSN: 0022-2836.
DT Article
LA English
AB This paper describes the detailed three-dimensional structures of two **zinc-finger** domains from the yeast transcription factor SWI5, calculated using the results of the n.m.r. experiments described in the accompanying paper. The structure of **finger** 2 is essentially similar to those previously obtained by others for isolated, synthetic single **zinc-finger** domains in solution, and for the three **zinc-finger peptide** Zif268 in its crystalline complex with **DNA**. The N-terminal half of the

sequence forms a two-stranded, irregular beta-sheet containing both the metal-**binding** cysteine residues, while the remainder of the structure forms a helix. Approximately the first half of this helix is alpha-helical, whereas the C-terminal portion, including the two metal **binding** histidine residues, is 3-10 helical. Four invariant hydrophobic residues form a core to the structure. In contrast to all previously described structures of **zinc-finger** domains, **finger** 1 has an additional strand in the beta-sheet, formed by residues N-terminal to the formal start of the **finger** motif. This additional strands plays a role in stabilising the folded form of **finger** 1, since a two-**finger peptide** lacking the N-terminal residues showed folded structure in **finger** 2 but not in **finger** 1.

CC Genetics and Cytogenetics - Plant *03504
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - Molecular Properties and Macromolecules *10506
BC Fungi - Unspecified *15000
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics
IT Miscellaneous Descriptors
DNA BINDING PROTEIN; NMR; THREE DIMENSIONAL STRUCTURE; TRANSCRIPTION ACTIVATOR **PROTEIN**
ORGN Super Taxa
Fungi - Unspecified: Fungi, Plantae
ORGN Organism Name
fungi (Fungi - Unspecified); yeast (Fungi - Unspecified)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants

L74 ANSWER 49 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1990:414201 BIOSIS
TI MODE OF INTERACTION OF THE **ZINC FINGER** PROTEIN TFIIIA WITH A 5S RNA GENE OF XENOPUS.
AU CHURCHILL M E A; TULLIUS T D; **KLUG A**
CS MEDICAL RES. COUNCIL LAB. MOL., HILLS RD., CAMBRIDGE CB2 2QH, ENGLAND.
SO PROC NATL ACAD SCI U S A, (1990) 87 (14), 5528-5532.
CODEN: PNASA6. ISSN: 0027-8424.
FS BA; OLD
LA English
AB The **zinc finger protein** TFIIIA, a positive transcription factor of the 5S RNA gene, binds to an internal control region of 50 nucleotides. Two modes of **binding** have been considered for the TFIIIA-**DNA** complex, one of which has beef proposed on the basis of nuclease and chemical protection experiments and the other on model building. Since then, evidence has accumulated on the structures of individual components of the complex-for example, zinc **finger polypeptides studied** by NMR and a segment of the binding **site** analyzed by x-ray crystallography, but no high-resolution structural data on the TFIIIA-DNA **complex** itself are available. Probes used previously to study the TFIIIA-DNA **complex** do not react with every nucleotide of DNA, **unlike** hydroxyl radical, which cleaves DNA **at** every backbone position. We describe here the quantitative analysis of high-resolution hydroxyl radical footprints and suggest how the array of zinc **fingers** **might** interact with the double helix.

CC Genetics and Cytogenetics - Animal *03506
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines 10052
Biochemical Methods - Proteins, Peptides and Amino Acids 10054
Biochemical Methods - Minerals 10059
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - Minerals *10069
Biophysics - Molecular Properties and Macromolecules *10506
BC Salientia 85306
IT Miscellaneous Descriptors